

STIC-BioTech/ChemLib

195815

From: Ramirez, Delia  
Sent: Monday, July 17, 2006 11:19 PM  
To: STIC-BioTech/ChemLib  
Subject: 10/716470

Hi,

I would like to request the following search: SEQ ID NO:10 in the protein databases (commercial & interference).

Thank you very much,

Delia M. Ramirez, Ph.D.  
Patent Examiner  
Recombinant Enzymes-Art Unit 1652  
USPTO  
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70  
Alexandria, VA 22314  
(571) 272-0938  
delia.ramirez@uspto.gov

CNFE

78701

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2006, 00:21:48 ; Search time 202 Seconds  
(without alignments)  
280.668 Million cell updates/sec

Title: US-10-716-470-10

Perfect score: 620  
Sequence: 1 NWIMEIFITGLIGASLLS.....EETPTVPDDTPIGVFGGH 124

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1980s:\*  
3: geneseqp2000s:\*  
4: geneseqp2000s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	620	100.0	124	6	ABR58214
2	620	100.0	124	8	AD033791
3	620	100.0	124	8	AD027294
4	620	100.0	124	8	ADR89160
5	584	94.2	236	2	AAW37715
6	584	94.2	236	4	AAW37715
7	584	94.2	236	6	ABR58213
8	584	94.2	236	8	AD033789
9	584	94.2	236	8	AD033895
10	584	94.2	236	8	AD027292
11	584	94.2	236	8	ADR19717
12	576	93.4	236	8	ADR89158
13	576	92.9	236	8	AD033908
14	571	92.1	233	4	AAU71888
15	571	92.1	233	4	AAU71888
16	571	92.1	233	7	ADB66197
17	389.5	62.8	231	4	AA664047
18	213	34.4	211	9	AB017795
19	213	34.4	211	9	AB017795
20	213	34.4	211	9	AB017795
21	213	34.4	211	9	AB017795
22	205	33.1	213	9	AB065328
23	185	23.8	214	7	ADP04687

24	176	28.4	208	6	ABM68839	ABM68839	Phototax
25	172.5	27.8	232	7	ABO75733	ABO75733	Pseudomon
26	170	27.4	199	7	ADG15729	ADG15729	M. tubercu
27	169	27.3	213	9	ABE36584	ABE36584	L. pneumo
28	165	26.6	201	9	ABE39976	ABE39976	L. pneumo
29	158	25.5	211	6	ADA34450	ADA34450	Acinetoba
30	112	18.1	211	9	ABM90714	ABM90714	M. xanthu
31	109	17.6	219	7	ABO61214	ABO61214	Klebsiell
32	104	16.8	212	8	AD051700	AD051700	Streptomy
33	101.5	16.4	205	6	ABM72206	ABM72206	Staphyloc
34	99.5	16.0	212	7	ADF04482	ADF04482	Bacterial
35	97	15.6	205	6	ABM67507	ABM67507	Phototax
36	97	15.6	222	9	AEAD4854	AEAD4854	S. tenjim
37	93.5	15.1	235	6	ADA36962	ADA36962	Acinetoba
38	93	15.0	211	6	ABU19902	ABU19902	Protein e
39	91	14.7	111	2	AAW89961	AAW89961	Antigen f
40	91	14.7	210	2	AAW20426	AAW20426	H. pylori
41	91	14.7	215	2	AAW20968	AAW20968	H. pylori
42	91	14.7	252	8	ADY09559	ADY09559	Plant ful
43	90.5	14.6	208	6	ADA33824	ADA33824	Acinetoba
44	88.5	14.3	212	3	ABO17787	ABO17787	Escherich
45	88.5	14.3	212	9	ABO7791	ABO7791	Escherich

## ALIGNMENTS

RESULT 1	ABR58214	standard; protein; 124 AA.
ID	ABR58214	
XX	ABR58214	
AC	ABR58214	
XX	ABR58214	
DT	23-OCT-2003	(revised)
DT	11-AUG-2003	(first entry)
XX	LYSE24 protein.	
DE	LYSE24 protein.	
XX	LYSE24 protein.	
KM	L-lysine; L-arginine; LYSE24.	
OS	Corynebacterium glutamicum.	
XX	Corynebacterium glutamicum.	
PN	EP1266966-A2.	
XX	EP1266966-A2.	
PD	18-DEC-2002.	
XX	18-DEC-2002.	
PF	05-JUN-2002; 2002EP-00012539.	
XX	05-JUN-2002; 2002EP-00012539.	
PR	12-JUN-2001; 2001JP-00177075.	
XX	12-JUN-2001; 2001JP-00177075.	
PA	(AJIN ) AJINOMOTO CO INC.	
PI	(AJIN ) AJINOMOTO CO INC.	
XX	(AJIN ) AJINOMOTO CO INC.	
PI	Gunji Y, Yasueda H;	
XX	Gunji Y, Yasueda H;	
DR	WPI; 2003-241171/24.	
XX	WPI; 2003-241171/24.	
DR	N-PSDB; ACC80942.	
XX	N-PSDB; ACC80942.	
PT	Novel DNA encoding variant of lyse protein from a coryneform bacterium,	
PT	when introduced into methanol assimilating bacterium, facilitates	
PT	excretion of L-lysine and/or L-arginine to outside of a cell.	
PS	Claim 8; Page 20; 23pp; English.	
XX	Claim 8; Page 20; 23pp; English.	
CC	The present invention relates to DNA encoding variants of protein with	
CC	loop region and six hydrophobic helices which facilitates excretion of L-	
CC	lysine and/or L-arginine to outside of cell of a methanol assimilating	
CC	bacterium when introduced into the bacterium. The method is used for	
CC	encoding a protein which facilitates excretion of L-lysine, L-arginine or	
CC	both of these L-amino acids to outside of a cell of a methanol	
CC	assimilating bacterium when DNA of the method is introduced into the	
CC	bacterium. The present sequence represents a lyse24 protein from	
CC	Brevibacterium lactofermentum. (Updated on 23-OCT-2003 to standardise OS	
CC	field)	

XX Sequence 124 AA;  
 SQ Query Match 100.0%; Score 620; DB 6; Length 124;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-68;  
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 MVMEIFITGLLGASLLSISGPQNVLYIKQIKREGIAYLVCLISDVFLFTAGTLGV 60  
 1 MVMEIFITGLLGASLLSISGPQNVLYIKQIKREGIAYLVCLISDVFLFTAGTLGV 60  
 61 DLISNAAPIVLDIMRWGIAVLLWFAVMAKADMTNKVEAPQIIETEPTVPDDTPIGVF 120  
 61 DLISNAAPIVLDIMRWGIAVLLWFAVMAKADMTNKVEAPQIIETEPTVPDDTPIGVF 120  
 121 GGGH 124  
 121 GGGH 124  
 Db 121 GGGH 124

## RESULT 2

ADO33791  
 ID ADO33791 standard; protein; 124 AA.

AC ADO33791;  
 XX

DT 12-AUG-2004 (first entry)  
 XX

DE Corynebacterium glutamicum lysE (lysine export) mutant lysE24 protein.  
 XX

KM lysE; lysine export; L-Lys production; L-Arg; methanol; mutant; mutein;  
 XX

lysE24.  
 XX

OS Corynebacterium glutamicum.  
 XX

OS Synthetic;  
 XX

Key Location/Qualifiers  
 XX

FT Misc-difference 119..124  
 XX

FT /note="Replace wild-type residues 119-233 as a result of  
 XX lysE24 mutation within coding DNA"

PN FR2847262-A1.  
 XX

PD 21-MAY-2004.  
 XX

PF 20-NOV-2003; 2003FR-00013575.  
 XX

PR 20-NOV-2002; 2002JP-00336340.  
 XX

PA (AJIN ) AJINOMOTO CO INC.  
 XX

PI Gunji Y, Yasueda H;  
 XX

DR MPI: 2004-403035/38.  
 XX

DR N-PSDB; ADO33790.  
 XX

PT Methylobacillus organism, useful for producing lysine and arginine,  
 PT contains DNA encoding variant form of lysE protein that contains only the  
 PT hydrophobic helices.  
 XX

PS Claim 5; SEQ ID NO 10; 49pp; French.  
 XX

XX The invention relates to a novel bacterium of the genus Methylobacillus  
 CC that contains a DNA encoding a variant of the lysE (lysine export)  
 CC protein and is able to produce L-Lys or L-Arg. The bacterium of the  
 CC invention may be useful for production of L-Lys or L-Arg since  
 CC incorporation of the lysE variant induces secretion of Lys and Arg, thus  
 CC improving productivity. The bacterium can be grown on methanol, an  
 CC inexpensive carbon source. The wild-type lysE protein is lethal to  
 CC methanol-utilizing bacteria. The current sequence is that of the  
 CC Corynebacterium glutamicum lysE (lysine export) mutant lysE24 protein of  
 CC the invention.  
 XX

SQ Sequence 124 AA;  
 SQ Query Match 100.0%; Score 620; DB 8; Length 124;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-68;  
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 MVMEIFITGLLGASLLSISGPQNVLYIKQIKREGIAYLVCLISDVFLFTAGTLGV 60  
 1 MVMEIFITGLLGASLLSISGPQNVLYIKQIKREGIAYLVCLISDVFLFTAGTLGV 60  
 61 DLISNAAPIVLDIMRWGIAVLLWFAVMAKADMTNKVEAPQIIETEPTVPDDTPIGVF 120  
 61 DLISNAAPIVLDIMRWGIAVLLWFAVMAKADMTNKVEAPQIIETEPTVPDDTPIGVF 120  
 121 GGGH 124  
 121 GGGH 124  
 Db 121 GGGH 124

## RESULT 3

ADO27294  
 ID ADO27294 standard; protein; 124 AA.

AC ADO27294;  
 XX

DT 12-AUG-2004 (first entry)  
 XX

DE Mutant Corynebacterium glutamicum truncated lysE protein Segid 10.  
 XX

KM Entner-Doudoroff pathway; methanol metabolism;  
 XX 6-phosphogluconate dehydratase; EDP;

KM 2-keco-3-deoxy-6-phosphogluconate aldolase; EDA; L-amino acid;  
 XX agriculture; food industry; lysE; mutant; mutein.

XX Corynebacterium glutamicum.  
 XX

OS Synthetic.  
 XX

PN FR2847265-A1.  
 XX

PD 21-MAY-2004.  
 XX

PF 20-NOV-2003; 2003FR-00013576.  
 XX

PR 20-NOV-2002; 2002JP-00336346.  
 XX

PA (AJIN ) AJINOMOTO CO INC.  
 XX

PI Gunji Y, Yasueda H;  
 XX

DR MPI: 2004-403038/38.  
 XX

DR N-PSDB; ADO27293.  
 XX

PT Microbial production of amino acids, useful in agriculture and foods,  
 PT comprises growing bacteria that use the Entner-Doudoroff pathway for  
 PT methanol metabolism and have increased activity of enzymes in this  
 PT pathway.  
 XX

PS Disclosure; SEQ ID NO 10; 51pp; French.  
 XX

XX This invention relates to the novel production of L-amino acids from  
 CC microorganisms that use the Entner-Doudoroff pathway for methanol  
 CC metabolism, such that L-residues are secreted into and recovered from the  
 CC culture medium. Specifically, it refers to an increase in the activity of  
 CC two enzymes, namely 6-phosphogluconate dehydratase (EDP) and/or 2-keco-3  
 CC -deoxy-6-phosphogluconate aldolase (EDA) that improve production of  
 CC certain amino acids from an inexpensive carbon source. The present  
 CC invention describes the production of L-amino acids from a biosynthetic  
 CC pathway that uses pyruvic acid as an intermediate. Accordingly, this  
 CC method can be used to produce lysine, leucine, isoleucine and valine,  
 CC which are amino acids applicable to the agricultural and food industries.  
 CC This polypeptide sequence is the mutant Corynebacterium glutamicum lysE  
 CC protein containing an in frame stop codon that truncates the protein  
 CC prematurely, given in an exemplification of the invention.

XX Sequence 124 AA;  
 SQ Query Match 100.0%; Score 620; DB 8; Length 124;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-68;  
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MWIMEIFITGLLGASLLSIGPQNVLVIKGIRKGLIAVLVCLISDVFLFIAGTLGV 60  
 DB 1 MWIMEIFITGLLGASLLSIGPQNVLVIKGIRKGLIAVLVCLISDVFLFIAGTLGV 60  
 QY 61 DLSNNAPIVLDIMRWGIAVLLMFPAWMAKADMTNKVEAPOIIEETEPVDDPDLGVF 120  
 DB 61 DLSNNAPIVLDIMRWGIAVLLMFPAWMAKADMTNKVEAPOIIEETEPVDDPDLGVF 120  
 QY 121 GGGH 124  
 DB 121 GGGH 124  
 RESULT 4  
 ADR89160  
 ID ADR89160 standard; protein; 124 AA.  
 XX ADR89160;  
 AC 18-NOV-2004 (first entry)  
 DT  
 DE Amino acid sequence of a mutant lysE gene fragment.  
 XX  
 KM lysine decarboxylase; enzyme; ldc gene; lysine; cadaverine; L-lysine;  
 KM lysine production; lysE gene.  
 XX  
 OS Corynebacterium glutamicum.  
 OS Synthetic.  
 XX  
 PN FR2851575-A1.  
 PD 27-AUG-2004.  
 XX  
 PF 25-FEB-2004; 2004FR-00001873.  
 XX  
 PR 25-FEB-2003; 2003JP-00047185.  
 XX  
 PA (AJIN ) AJINOMOTO CO INC.  
 XX  
 PI Hirano S, Yasueda H;  
 XX  
 DR WPI; 2004-618218/60.  
 DR N-PSDB; ADR89159.  
 XX  
 PT Preparation of L-lysine by growing Methylobionas in which the endogenous  
 PT lysine decarboxylase gene has been inactivated, also new lysine  
 PT decarboxylase and nucleic acid encoding it.  
 XX  
 PS Example 4; SEQ ID NO 24; 57bp; French.  
 XX  
 CC The specification describes a lysine decarboxylase enzyme of  
 CC Methylobionas methylotrophus. The lysine decarboxylase gene is designated  
 CC ldc gene. The lysine decarboxylase enzyme decomposes lysine to  
 CC cadaverine. M. methylotrophus cells in which this gene has been reduced  
 CC or eliminated are useful for fermentative production of L-lysine in  
 CC methanol-based media. Inactivation of the enzyme increases the efficiency  
 CC of lysine production in Methylobionas cells. The present sequence is  
 CC encoded by a mutated lysE gene fragment, with a thymine inserted after  
 CC guanine 355. This fragment was used to construct a plasmid which was then  
 CC used to produce L-lysine in cells containing an interrupted ldc gene.  
 XX  
 SQ Sequence 124 AA;  
 Query Match 100.0%; Score 620; DB 8; Length 124;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-68;  
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWIMEIFITGLLGASLLSIGPQNVLVIKGIRKGLIAVLVCLISDVFLFIAGTLGV 60  
 DB 1 MWIMEIFITGLLGASLLSIGPQNVLVIKGIRKGLIAVLVCLISDVFLFIAGTLGV 60  
 QY 61 DLSNNAPIVLDIMRWGIAVLLMFPAWMAKADMTNKVEAPOIIEETEPVDDPDLGVF 120  
 DB 61 DLSNNAPIVLDIMRWGIAVLLMFPAWMAKADMTNKVEAPOIIEETEPVDDPDLGVF 120  
 QY 121 GGGH 124  
 DB 121 GGGH 124  
 RESULT 5  
 AAW37715  
 ID AAW37715 standard; protein; 236 AA.  
 XX AAW37715;  
 AC 12-MAR-1998 (first entry)  
 DT  
 DE C. glutamicum Lys E protein (lysine export protein).  
 XX  
 KM lysE; lysE; ORF3; lysine transport; regulatory protein; export protein;  
 KM microbial production; amino acid; animal feed additive.  
 XX  
 OS Corynebacterium glutamicum.  
 PN DE19548222-A1.  
 PD 26-JUN-1997.  
 XX  
 PF 22-DEC-1995; 95DE-01048222.  
 XX  
 PR 22-DEC-1995; 95DE-01048222.  
 XX  
 PA (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.  
 XX  
 PI Vrijic M, Eggeling L, Sahm H;  
 XX  
 DR WPI; 1997-333867/31.  
 DR N-PSDB; AAT96816.  
 XX  
 PT Increasing microbial production of amino acids, especially lysine - by  
 PT improving export carrier activity or corresponding gene expression, also  
 PT new export and regulatory genes from Corynebacterium.  
 XX  
 PS Claim 42; Page 10; 16pp; German.  
 XX  
 CC This sequence is the lysE protein product, a lysine export protein. lysE  
 CC and lysE encode a lysine transport regulatory protein and an export  
 CC protein, respectively. Microbial production of amino acids (A) is  
 CC improved by increasing the export-carrier activity and/or the export gene  
 CC expression in a microorganism that produces (A). The method is  
 CC specifically used to increase production of lysine, used as an animal  
 CC feed additive. Other (A) are variously useful as pharmaceuticals,  
 CC condiments and intermediates for fine chemicals. This method increases  
 CC the amount of (A) secreted into the culture medium. Export of (A) has  
 CC been found to depend on a single gene  
 XX  
 SQ Sequence 236 AA;  
 Query Match 94.2%; Score 584; DB 2; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-63;  
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MWIMEIFITGLLGASLLSIGPQNVLVIKGIRKGLIAVLVCLISDVFLFIAGTLGV 60  
 DB 1 MWIMEIFITGLLGASLLSIGPQNVLVIKGIRKGLIAVLVCLISDVFLFIAGTLGV 60  
 QY 61 DLSNNAPIVLDIMRWGIAVLLMFPAWMAKADMTNKVEAPOIIEETEPVDDPDLGVF 118

DB 61 DLNSNAPIVLDIRMGIAVLLMFVMAKADMTNKVEAPQIETEPTVPDDTFLG 118

RESULT 6  
AAG93201  
ID AAG93201 standard; procein; 236 AA.  
XX  
AC AAG93201;  
XX  
DT 26-SEP-2001 (first entry)  
XX  
DE C glutamicum protein fragment SEQ ID NO: 6955.  
XX  
KM Coryneform bacterium; amino acid synthesis; vitamin; saccharide;  
XX organic acid synthesis.  
XX  
OS Corynebacterium glutamicum.  
XX  
PN EPI108790-A2.  
XX  
PD 20-JUN-2001.  
XX  
PF 18-DEC-2000; 2000EP-00127688.  
XX  
PR 16-DEC-1999; 99JP-00377484.  
XX 07-APR-2000; 2000JP-00159162.  
XX 03-AUG-2000; 2000JP-00280988.  
XX  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;  
XX Tateishi N, Senoh A, Ikeda M, Ozaki A;  
XX  
XX WPI; 2001-376931/40.  
XX N-PSDB; AAH68420.  
XX  
DR  
XX  
XX Novel polynucleotides derived from Coryneform bacteria, for identifying  
XX mutation point of a gene, measuring expression of a gene, analyzing  
XX expression profile or pattern of a gene and identifying homologous gene.  
XX  
XX Claim 29; SEQ ID NO 6955; 246bp + Sequence Listing; English.  
XX  
XX The present invention provides a number of nucleotide and protein  
XX sequences from the Coryneform bacterium Corynebacterium glutamicum. These  
XX are useful for identifying the mutation point of a gene derived from a  
XX mutant of coryneform bacterium, measuring expression amount and analyzing  
XX the expression profile or expression pattern of a gene derived from  
XX Coryneform bacterium, and identifying a homologue of a gene derived from  
XX Coryneform bacterium. Coryneform bacteria are useful for producing amino  
XX acids, nucleic acids, vitamins, saccharides and organic acids,  
XX particularly L-lysine. The present sequence is a protein described in the  
XX exemplification of the invention. Note: The sequence data for this patent  
XX did not form part of the printed specification, but was obtained in  
XX electronic format directly from the European Patent Office

XX  
XX Sequence 236 AA:  
XX  
XX Query Match 94.2%; Score 584; DB 4; Length 236;  
XX Best Local Similarity 100.0%; Pred. No. 1.9e-63;  
XX Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTMEFITGLLIGASLLSIGPQNVLYIKGIRKGLAVLLVCLISDVFLFIAGTLGV 60  
DB 1 MVTMEFITGLLIGASLLSIGPQNVLYIKGIRKGLAVLLVCLISDVFLFIAGTLGV 60  
QY 61 DLNSNAPIVLDIRMGIAVLLMFVMAKADMTNKVEAPQIETEPTVPDDTFLG 118  
DB 61 DLNSNAPIVLDIRMGIAVLLMFVMAKADMTNKVEAPQIETEPTVPDDTFLG 118

RESULT 7  
ABR58213  
ID ABR58213 standard; protein; 236 AA.

XX  
XX ABR58213;  
XX  
XX 23-OCT-2003 (revised)  
XX 11-AUG-2003 (first entry)  
XX  
XX LysE protein.  
XX  
XX L-lysine; L-arginine; LysE.  
XX  
XX Corynebacterium glutamicum.  
XX  
XX EPI266966-A2.  
XX  
XX 18-DEC-2002.  
XX  
XX 05-JUN-2002; 2002EP-00012539.  
XX  
XX 12-JUN-2001; 2001JP-00177075.  
XX  
XX (AJIN ) AJINOMOTO CO INC.  
XX  
XX Gunji Y, Yasueda H;  
XX  
XX WPI; 2003-241171/24.  
XX N-PSDB; ACC80941.  
XX  
XX Novel DNA encoding variant of LysE protein from a coryneform bacterium,  
XX when introduced into methanol assimilating bacterium, facilitates  
XX excretion of L-lysine and/or L-arginine to outside of a cell.  
XX  
XX Disclosure; Page 18-19; 23pp; English.  
XX  
XX The present invention relates to DNA encoding variants of protein with  
XX loop region and six hydrophobic helices which facilitates excretion of L-  
XX lysine and/or L-arginine to outside of cell of a methanol assimilating  
XX bacterium when introduced into the bacterium. The method is used for  
XX encoding a protein which facilitates excretion of L-lysine, L-arginine or  
XX both of these L-amino acids to outside of a cell of a methanol  
XX assimilating bacterium when DNA of the method is introduced into the  
XX bacterium. The present sequence represents a LysE protein from  
XX Brevibacterium lactofermentum. (Updated on 23-Oct-2003 to standardise OS  
XX field)

XX  
XX Sequence 236 AA:  
XX  
XX Query Match 94.2%; Score 584; DB 6; Length 236;  
XX Best Local Similarity 100.0%; Pred. No. 1.9e-63;  
XX Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTMEFITGLLIGASLLSIGPQNVLYIKGIRKGLAVLLVCLISDVFLFIAGTLGV 60  
DB 1 MVTMEFITGLLIGASLLSIGPQNVLYIKGIRKGLAVLLVCLISDVFLFIAGTLGV 60  
QY 61 DLNSNAPIVLDIRMGIAVLLMFVMAKADMTNKVEAPQIETEPTVPDDTFLG 118  
DB 61 DLNSNAPIVLDIRMGIAVLLMFVMAKADMTNKVEAPQIETEPTVPDDTFLG 118

RESULT 8  
ADO33789  
ID ADO33789 standard; protein; 236 AA.  
XX  
XX ADO33789;  
XX  
XX 12-AUG-2004 (first entry)  
XX  
XX Corynebacterium glutamicum LysE (lysine export) wild-type protein.  
XX  
XX LysE; lysine export; L-Lys production; L-Arg; methanol; wild-type.  
XX  
XX Corynebacterium glutamicum.  
XX

PN	FR2847262-A1.
XX	
PD	21-MAY-2004.
XX	
PF	20-NOV-2003; 2003FR-00013575.
XX	
PR	20-NOV-2002; 2002JP-00336340.
XX	
PA	(AJIN ) AJINOMOTO CO INC.
XX	
P1	Gunji Y, Yasueda H;
XX	
DR	WPI, 2004-403035/38.
N-PSDB:	ADO33788.
XX	
PT	Methylobacillus organism, useful for producing lysine and arginine,
FT	contains DNA encoding variant form of LysE protein that contains only the
XX	hydrophobic helices.
PS	Example 1; SEQ ID NO 8; 49pp; French.
XX	
CC	The invention relates to a novel bacterium of the genus Methylobacillus
CC	that contains a DNA encoding a variant of the LysE (lysine export)
CC	protein and is able to produce L-Lys or L-Arg. The bacterium of the
CC	invention may be useful for production of L-Lys or L-Arg since
CC	incorporation of the LysE variant induces secretion of Lys and Arg, thus
CC	improving productivity. The bacterium can be grown on methanol, an
CC	expensive carbon source. The wild-type LysE protein is lethal to
CC	methanol-utilizing bacteria. The current sequence is that of the
CC	Corynebacterium glutamicum LysE (lysine export) wild-type protein of the
XX	invention.
SQ	Sequence 236 AA;
Query Match	94.2%; Score 584; DB 8; Length 236;
Best local similarity	100.0%; Pred. No. 1.9e-63;
Matches 118; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MWIEIFITGLLGSLLSIGPQNVLYIKQGIKREGIAVLVCLISDVEFLIAGTLGV 60
DB	1 MWIEIFITGLLGSLLSIGPQNVLYIKQGIKREGIAVLVCLISDVFLFINGTIGV 60
QY	61 DLLSNAAPIVLDIMRWGSIAYILMFAVMAADAMTKKEAPDIETETPTVPDDTPLG 118
DB	61 DLLSNAAPIVLDIMRWGSIAYILMFAVMAADAMTKKEAPDIETETPTVPDDTPLG 118
RESULT 9	
ID	ADO33895 standard; protein; 236 AA.
AC	ADO33895;
XX	
DT	12-AUG-2004 (first entry)
XX	
DE	Corynebacterium glutamicum LysE (lysine export) wild-type protein.
XX	
KM	LysE, lysine export; methanol-utilising bacterium;
XX	S-(2-aminoethyl)cysteine resistance; arginine export; wild-type.
OS	Corynebacterium glutamicum.
PN	FR2847264-A1.
XX	
FD	21-MAY-2004.
XX	
PF	20-NOV-2003; 2003FR-00013574.
XX	
PR	20-NOV-2002; 2002JP-00336345.
XX	
PA	(AJIN ) AJINOMOTO CO INC.
XX	
I1	Gunji Y, Yasueda H;

XX WP1: 2004-403037/38.  
DR N-PSDB; ADO03894.  
XX  
XX New DNA encoding mutant form of Lyse protein, useful for transformation  
PT of methanol-utilizing bacteria for production of lysine and arginine,  
XX also new transformants.  
XX  
PS Claim 1; SEQ ID NO 2; 52pp; French.  
XX  
CC The invention relates to a novel DNA that encodes a mutant of the Lyse  
CC (lysine export) protein of a corynebacterium, or its homologue, in  
CC which at least gly55 has been replaced by a different amino acid and  
CC where the introduction of the DNA into a methanol-utilizing bacterium  
CC confers resistance to a lysine analogue such as S-(2-aminoethyl) cysteine.  
CC The DNA of the invention may be useful since its introduction induces  
CC export of lys and/or Arg from cells, thus facilitating production of  
CC these amino acids from an inexpensive carbon source and increasing their  
CC concentration in the extracellular medium. The wild-type Lyse sequence is  
CC not functional in methanol-utilizing bacteria. The current sequence is  
CC that of the Corynebacterium glutamicum Lyse (lysine export) wild-type  
CC protein of the invention.  
XX  
SQ Sequence 236 AA;  
XX  
Query Match 94.2%; Score 584; DB 8; Length 236;  
Best Local Similarity 100.0%; Pred. No. 1.9e-63;  
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 MWMEIFITGLLGASLLLSIGPQNVLVIKGIRREGILAVLVCLISDVFLFIAGTLGV 60  
Db 1 MWMEIFITGLLGASLLLSIGPQNVLVIKGIRREGILAVLVCLISDVFLFIAGTLGV 60  
Oy 61 DLSNAPPIVLDIMRKGIAIYLLMFAPMAKADANTNKVEAPQIIIEETEPVPDDTPIG 118  
Db 61 DLSNAPPIVLDIMRKGIAIYLLMFAPMAKADANTNKVEAPQIIIEETEPVPDDTPIG 118  
RESULT 10  
ADO27292  
ID ADO27292 standard; protein; 236 AA.  
XX  
AC ADO27292;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Corynebacterium glutamicum lyse protein segid 8.  
XX  
KW Entner-Doudoroff pathway; methanol metabolism;  
KW 6-phosphogluconate dehydratase; EDD;  
KW 2-keto-3-deoxy-6-phosphogluconate aldolase; EDA; L-amino acid;  
XX agriculture; food industry; lyse.  
XX  
OS Corynebacterium glutamicum.  
XX  
XX FR2847265-A1.  
XX  
XX 21-MAY-2004.  
XX  
XX 20-NOV-2003; 2003FR-00013576.  
XX  
XX 20-NOV-2002; 2002JP-00336346.  
XX  
XX (AJIN ) AJINOMOTO CO INC.  
XX  
XX Gunji Y, Yasueda H;  
XX  
XX WP1: 2004-403038/38.  
XX  
XX N-PSDB; ADO27291.  
XX  
XX  
XX Microbial production of amino acids, useful in agriculture and foods,  
XX comprises growing bacteria that use the Entner-Doudoroff pathway for  
XX methanol metabolism and have increased activity of enzymes in this  
XX pathway.

PT pathway.  
 XX  
 PS Disclosure; SEQ ID NO 8; s1pp; French.  
 XX  
 CC This invention relates to the novel production of L-amino acids from  
 CC microorganisms that use the Entner-Doudoroff pathway for methanol  
 CC metabolism, such that L-residues are secreted into and recovered from the  
 CC culture medium. Specifically, it refers to an increase in the activity of  
 CC two enzymes, namely 6-phosphogluconate dehydratase (EDD) and/or 2-keto-3  
 CC -deoxy-6-phosphogluconate aldolase (EDA) that improve production of  
 CC certain amino acids from an inexpensive carbon source. The present  
 CC invention describes the production of L-amino acids from a biosynthetic  
 CC pathway that uses pyruvic acid as an intermediate. Accordingly, this  
 CC method can be used to produce lysine, leucine, isoleucine and valine,  
 CC which are amino acids applicable to the agricultural and food industries.  
 CC This polypeptide sequence is the Corynebacterium glutamicum lysE protein  
 CC given in an exemplification of the invention.  
 CC  
 XX Sequence 236 AA;  
 SQ  
 Query Match 94.2%; Score 584; DB 8; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-63;  
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MVIMEIFITGLLGASLLSIGPQNVLYIKGIRKREGLIIVLVCLISDVFLFIAGTLGV 60  
 Db 1 MVIMEIFITGLLGASLLSIGPQNVLYIKGIRKREGLIIVLVCLISDVFLFIAGTLGV 60  
 QY 61 DLISNAPIVLDIMRWGIAVLLMFVMAAKDAMTKVKAPOIIEETEPVPDDTPIG 118  
 Db 61 DLISNAPIVLDIMRWGIAVLLMFVMAAKDAMTKVKAPOIIEETEPVPDDTPIG 118  
 RESULT 11  
 ADRI9717  
 ID ADRI9717 standard; protein; 236 AA.  
 XX  
 AC ADRI9717;  
 XX  
 DT 21-OCT-2004 (first entry)  
 XX  
 DE lysE amino acid sequence, seq id 18.  
 XX  
 KM L-lysine; bacteria; methanol; L-methionine; Methylophilus bacteria; meta;  
 XX homoserine o-acetyltransferase; lysE.  
 XX  
 OS Corynebacterium glutamicum.  
 XX  
 PN FR2850394-A1.  
 XX  
 PD 30-JUL-2004.  
 XX  
 PF 29-JAN-2004; 2004FR-00000816.  
 XX  
 PR 29-JAN-2003; 2003JP-00020513.  
 XX  
 PA (AJIN ) AJINOMOTO CO INC.  
 XX  
 DR MPI; 2004-563572/55.  
 DR N-PADB; ADRI9716.  
 XX  
 PT L-lysine preparation with high productivity, by culturing methanol-  
 PT utilizing bacteria auxotrophic for L-methionine, preferably new  
 PT Methylophilus strains.  
 XX  
 PS Disclosure; SEQ ID NO 18; 43pp; French.  
 XX  
 CC The invention relates to the production of L-lysine (I). The method  
 CC involves culturing bacteria which utilize methanol, require L-methionine  
 CC (II) for growth and produce (I) in a medium containing methanol as the  
 CC main carbon source, then recovering the (I) accumulated in the culture.  
 CC disclosed are Methylophilus bacteria which require (II) for growth and  
 CC produce (I). Methylophilus bacteria requiring (II) for growth are

CC obtained by mutation of wild strains using physical stimuli, or  
 CC preferably a chemical mutagen, or by using genetic engineering methods to  
 CC suppress the activity of an enzyme involved in the synthesis of (II),  
 CC e.g. by cleaving the gene metA (encoding homoserine o-acetyltransferase)  
 CC in Methylophilus methylotrophus. The invention is useful in the  
 CC production of L-lysine. L-lysine is obtained with high efficacy from  
 CC bacteria utilizing (inexpensive) methanol as carbon source. The current  
 CC sequence represents the lysE amino acid sequence.  
 CC  
 XX Sequence 236 AA;  
 SQ  
 Query Match 94.2%; Score 584; DB 8; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-63;  
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MVIMEIFITGLLGASLLSIGPQNVLYIKGIRKREGLIIVLVCLISDVFLFIAGTLGV 60  
 Db 1 MVIMEIFITGLLGASLLSIGPQNVLYIKGIRKREGLIIVLVCLISDVFLFIAGTLGV 60  
 QY 61 DLISNAPIVLDIMRWGIAVLLMFVMAAKDAMTKVKAPOIIEETEPVPDDTPIG 118  
 Db 61 DLISNAPIVLDIMRWGIAVLLMFVMAAKDAMTKVKAPOIIEETEPVPDDTPIG 118  
 RESULT 12  
 ADRI9158  
 ID ADRI9158 standard; protein; 236 AA.  
 XX  
 AC ADRI9158;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Amino acid sequence of a wild type lysE gene.  
 XX  
 KM lysine decarboxylase; enzyme; ldc gene; lysine; cadaverine; L-lysine;  
 XX lysine production; lysE gene.  
 XX  
 OS Corynebacterium glutamicum.  
 XX  
 PN FR2851575-A1.  
 XX  
 PD 27-AUG-2004.  
 XX  
 PF 25-FEB-2004; 2004FR-00001873.  
 XX  
 PR 25-FEB-2003; 2003JP-00047185.  
 XX  
 PA (AJIN ) AJINOMOTO CO INC.  
 XX  
 PI Hirano S, Yasueda H;  
 XX  
 DR MPI; 2004-618218/60.  
 DR N-PADB; ADRI9157.  
 XX  
 PT Preparation of L-lysine by growing Methylomonas in which the endogenous  
 PT lysine decarboxylase gene has been inactivated, also new lysine  
 PT decarboxylase and nucleic acid encoding it.  
 XX  
 PS Example 4; SEQ ID NO 22; 57pp; French.  
 XX  
 CC The specification describes a lysine decarboxylase enzyme of  
 CC Methylophilus methylotrophus. The lysine decarboxylase gene is designated  
 CC ldc gene. The lysine decarboxylase enzyme decomposes lysine to  
 CC cadaverine. M. methylotrophus cells in which this gene has been reduced  
 CC or eliminated are useful for fermentative production of L-lysine in  
 CC methanol-based media. Inactivation of the enzyme increases the efficiency  
 CC of lysine production in Methylophilus cells. The present sequence is  
 CC encoded by a lysE gene fragment. This fragment was used to construct a  
 CC plasmid which was then used to produce L-lysine in cells containing an  
 CC interrupted ldc gene.  
 XX  
 SQ Sequence 236 AA;

```

Query Match      93.4%; Score 579; DB 8; Length 236;
Best Local Similarity 99.2%; Pred. No. 7.9e-63;
Matches 117; Conservative 1; Mismatches 0; Indels 0; Gaps 0

Oy 1 MWMEIFITGLLLGASLLSIGPQNVIVKQIGKEGLIAVLVCLISDFELFIAGTLGV 60
Db 1 MWMEIFITGLLLGASLLSIGPQNVIVKQIGKEGLIAVLVCLISDFELFIAGTLGV 60
Oy 61 DLISNAPIVLDIRMGIVYLLMFAVMAAKDANTNKVEAPQIIIEETPTVPDDTPIG 118
Db 61 DLISNAPIVLDIRMGIVYLLMFAVMAAKDANTNKVEAPQIIIEETPTVPDDTPIG 118

RESULT 13
ADO33908 standard; protein; 236 AA.
XX ADO33908;
AC ADO33908;
XX ADO33908;
DT 12-AUG-2004 (first entry)
DE Corynebacterium glutamicum lysE (lysine export) mutant G56K protein.
XX lysE: lysine export; methanol-utilising bacterium;
XX S-(2-aminoethyl)cysteine resistance; arginine export; mutant; mutein.
XX Corynebacterium glutamicum.
OS Synthetic.
XX Key Location/Qualifiers
XX Misc-difference 56 /note= "wild-type Gly substituted by Lys"
FT FR2847264-A1.
PN 21-MAY-2004.
PD 20-NOV-2003; 2003FR-00013574.
XX 20-NOV-2002; 2002JP-0036315.
PR 20-NOV-2002; 2002JP-0036315.
XX (AJIN') AJINOMOTO CO INC.
PA Gunji Y, Yasueda H;
XX WPI; 2004-403037/38.
DR New DNA encoding mutant form of lysE protein, useful for transformation
PT of methanol-utilizing bacteria for production of lysine and arginine,
PT also new transformants.
XX Claim 3; Page; 52pp; French.
XX The invention relates to a novel DNA that encodes a mutant of the lysE
XX (lysine export) protein of a coryneform bacterium, or its homologue, in
XX which at least Gly56 has been replaced by a different amino acid and
XX where the introduction of the DNA into a methanol-utilising bacterium
XX confers resistance to a lysine analogue such as S-(2-aminoethyl)cysteine.
XX The DNA of the invention may be useful since its introduction induces
XX export of Lys and/or Arg from cells, thus facilitating production of
XX these amino acids from an inexpensive carbon source and increasing their
XX concentration in the extracellular medium. The wild-type lysE sequence is
XX not functional in methanol-utilising bacteria. The current sequence is
XX that of the Corynebacterium glutamicum lysE (lysine export) mutant G56K
XX protein of the invention. The current sequence is not shown within the
XX specification per se but was created by the indexer using information
XX given within claim 3.
XX Sequence 236 AA;
XX
Query Match      92.9%; Score 576; DB 8; Length 236;
Best Local Similarity 99.2%; Pred. No. 1.9e-62;
Matches 117; Conservative 0; Mismatches 1; Indels 0; Gaps 0

```

Oy		1	MVMEIFFTGLLQASLLLSIGFONVLVIKQG;KREGLLAVLVLCISVPLEFIAGTLAGV	60
Dd		1	MVMEIFRTGLLLGASLLLSIGFONVLVIKQGIKEGGLLAVLVLCISDVFLEFIAGTLAGV	60
Oy		61	DLLSNAAPIVLDIMRWGIAVYLLMFVMAKAQAMTKVEAPQIIETETPTVDPTPLG	118
Dd		61	DLLSNAAPIVLDIMRWGIAVYLLMPFVMAKAQAMTKVEAPQIIETETPTVDPTPLG	118
<hr/>				
RESULT 14				
ID	AAB79660		standard; protein; 233 AA.	
XX				
AC	AAB79660;			
XX				
DT	30-APR-2001	(first entry)		
XX				
DE	Corynebacterium glutamicum MP	protein sequence SEQ ID NO:54.		
XX				
KW	Corynebacterium glutamicum; metabolic pathway protein; MP protein;			
KM	fine chemical production; microorganism; organic acid; nucleoside;			
KW	nonproteogenic amino acid; purine base; pyrimidine base; nucleotide;			
KM	lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;			
KW	carbohydrate; aromatic compound; cofactor; polyketide; enzyme.			
XX				
OS	Corynebacterium glutamicum.			
PN	MO200100843-A2.			
XX				
PD	04-JAN-2001.			
XX				
PF	23-JUN-2000; 2000NO-IEB00923.			
XX				
PR	25-JUN-1999;	99US-0141031P.		
PR	01-JUL-1999;	99DE-01030476.		
PR	02-JUL-1999;	99US-0142101P.		
PR	08-JUL-1999;	99DE-01031415.		
PR	08-JUL-1999;	99DE-01031418.		
PR	08-JUL-1999;	99DE-01031419.		
PR	08-JUL-1999;	99DE-01031420.		
PR	08-JUL-1999;	99DE-01031424.		
PR	08-JUL-1999;	99DE-01031428.		
PR	08-JUL-1999;	99DE-01031434.		
PR	08-JUL-1999;	99DE-01031435.		
PR	08-JUL-1999;	99DE-01031443.		
PR	08-JUL-1999;	99DE-01031453.		
PR	08-JUL-1999;	99DE-01031457.		
PR	08-JUL-1999;	99DE-01031465.		
PR	08-JUL-1999;	99DE-01031478.		
PR	08-JUL-1999;	99DE-01031510.		
PR	08-JUL-1999;	99DE-01031541.		
PR	08-JUL-1999;	99DE-01031573.		
PR	08-JUL-1999;	99DE-01031592.		
PR	08-JUL-1999;	99DE-01031633.		
PR	08-JUL-1999;	99DE-01031634.		
PR	08-JUL-1999;	99DE-01031636.		
PR	08-JUL-1999;	99DE-01031638.		
PR	08-JUL-1999;	99DE-01032125.		
PR	08-JUL-1999;	99DE-01032126.		
PR	08-JUL-1999;	99DE-01032130.		
PR	08-JUL-1999;	99DE-01032166.		
PR	08-JUL-1999;	99DE-01032206.		
PR	08-JUL-1999;	99DE-01032222.		
PR	08-JUL-1999;	99DE-01032228.		
PR	08-JUL-1999;	99DE-01032229.		
PR	08-JUL-1999;	99DE-01032230.		
PR	14-JUL-1999;	99DE-01032922.		
PR	14-JUL-1999;	99DE-01032926.		
PR	14-JUL-1999;	99DE-01032928.		
PR	14-JUL-1999;	99DE-01033004.		
PR	14-JUL-1999;	99DE-01033005.		
PR	14-JUL-1999;	99DE-01033006.		
PR	12-AUG-1999;	99US-0148613P.		

PR	27-AUG-1999;	99DE-01040764.
PR	27-AUG-1999;	99DE-01040765.
PR	27-AUG-1999;	99DE-01040766.
PR	27-AUG-1999;	99DE-01040832.
PR	31-AUG-1999;	99DE-01041378.
PR	31-AUG-1999;	99DE-01041379.
PR	31-AUG-1999;	99DE-01041380.
PR	31-AUG-1999;	99DE-01041394.
PR	03-SEP-1999;	99DE-01041396.
PR	03-SEP-1999;	99DE-01042076.
PR	03-SEP-1999;	99DE-01042077.
PR	03-SEP-1999;	99DE-01042079.
PR	03-SEP-1999;	99DE-01042086.
PR	03-SEP-1999;	99DE-01042087.
PR	03-SEP-1999;	99DE-01042088.
PR	03-SEP-1999;	99DE-01042095.
PR	03-SEP-1999;	99DE-01042124.
PR	03-SEP-1999;	99DE-01042129.
PR	09-MAR-2000;	2000US-0187970P.
PA	(BAD1 ) BASF AG.	
XX		
XX	Pompejus M, Kroegeer B, Schroeder H, Zelder O, Haberman G;	
XX	WPI; 2001-137957/14.	
DR	N-PSDB; AAF71779.	
PT		
PT	Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway	
PT	proteins, useful for producing fine chemicals in microorganisms,	
PT	including organic acids, nonproteinogenic amino acids, and purine and	
PT	pyrimidine bases.	
PS	Claim 20; Page 234-235; 1737pp; English.	
PS		
XX		
XX	AA01753 to AA07230 encode the Corynebacterium glutamicum metabolic	
CC	pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP	
CC	nucleic acids are useful for the production of fine chemicals in	
CC	microorganisms, including organic acids, nonproteinogenic amino acids,	
CC	purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated	
CC	and unsaturated fatty acids, diols, carbohydrates, aromatic compounds,	
CC	vitamins, cofactors, polyketides and enzymes	
XX		
XX	Sequence 233 AA;	
XX		
XX	Query Match	92.1%; Score 571; DB 4; Length 233;
XX	Best Local Similarity	100.0%; Pred. No. 7, 6e-62;
XX	Matches 115; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	4 MEIPIITGLLGSLLISIGPQNVLYVKGKIKREGILAVLLVCLISDVFPIAGTGVDL 63	
DB	1 MEIPIITGLLGSLLISIGPQNVLYVKGKIKREGILAVLLVCLISDVFPIAGTGVDL 60	
OY	64 SNAAPIVLIDIMRWGIAVYLLMFVMAKADAMTKVAPQIIEETPTVPDDPTLG 116	
DB	61 SNAAPIVLIDIMRWGIAVYLLMFVMAKADAMTKVAPQIIEETPTVPDDPTLG 115	
XX		
XX	RESULT 15	
XX	AAU71888	
XX	AAU71888 standard; protein; 233 AA.	
XX	AAU71888;	
XX		
XX	26-FEB-2002 (first entry)	
DE		
DE	C. glutamicum metabolic pathway protein encoded by gene #23.	
XX		
KW	Metabolic pathway protein; MP; lysine biosynthesis pathway;	
KW	methionine biosynthesis pathway; large-scale production of fine chemical;	
XX	Corynebacterium diphtheriae; diphtheria.	
XX		
XX	Corynebacterium glutamicum.	
XX		

```

PN WO200166573-A2.
XX
XX 13-SEP-2001.
XX
XX 22-DEC-2000; 2000WO-IB002035.
XX
XX 09-MAR-2000; 2000US-0187970P.
XX
XX 23-JUN-2000; 2000US-00606740.
XX
XX (BADI ) BASF AG.
XX
XX Pompejus M, Kroegeer B, Schroeder H, Zelder O, Haberhauer G;
XX Kim J, Lee H, Hwang B;
XX
XX WPI; 2001-582269/65.
XX
XX N-PSDB; AAS96098.
XX
XX Nucleic acids encoding metabolic pathway proteins from Corynebacterium
XX glutamicum, useful for producing methionine and lysine in Corynebacterium
XX and Brevibacterium.
XX
XX Disclosure; Page 215-216; 316pp; English.
XX
XX The present invention relates to the isolation of novel Corynebacterium
XX glutamicum genes (AAS96073-AAS96132) encoding metabolic pathway (MP)
XX proteins. The metabolic pathway proteins of the invention include enzymes
XX involved in the lysine and methionine biosynthetic pathways. The
XX polynucleotide sequences of the invention can be used for the large-scale
XX production and/or modulation of expression of fine chemicals such as
XX lysine and methionine. The sequences of the invention may be used to
XX identify C. glutamicum and related organisms e.g. C. diptheriae in a
XX subject to detect diptheria. AAU71863-AAU71922 represent the novel C.
XX glutamicum metabolic pathway proteins of the invention
XX
XX
XX Sequence 233 AA;
XX
XX Query Match 92.1%; Score 571; DB 4; Length 233;
XX Best Local Similarity 100.0%; Pred. No. 7.6e-62;
XX Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX 4 MEIPIITGILLGASLLISTGPNVLYIKGIRREGIIVLVLCISDVLFITAGTGVLL 63
XX |||||
XX 1 MEIPIITGILLGASLLISTGPNVLYIKGIRREGIIVLVLCISDVLFITAGTGVLL 60
XX
XX 64 SNAAPIVVDIMRWGCIAYLLMFAVMAAADAMTNKVEAPQIIEETPEPTVPDDTPLG 118
XX |||||
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XX Search completed: July 19, 2006, 00:25:26
XX Job time : 206 secs

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OM protein - protein search, using sw model

Run on: July 19, 2006, 00:42:58 ; Search time 188 Seconds  
(without alignments)  
305.525 Million cell updates/sec

Title: US-10-716-470-10

Perfect score: 620

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	620	100.0	124	4	US-10-716-473-10
3	620	100.0	124	5	US-10-784-986-24
4	620	100.0	124	5	US-10-716-470-10
5	584	94.2	236	3	US-09-738-626-6955
6	584	94.2	236	4	US-10-166-142-8
7	584	94.2	236	4	US-10-716-473-8
8	584	94.2	236	4	US-10-716-480A-2
9	584	94.2	236	4	US-10-760-283-18
10	584	94.2	236	5	US-10-784-986-22
11	584	94.2	236	5	US-10-716-470-8
12	571	92.1	233	3	US-09-746-660A-52
13	571	92.1	233	4	US-10-196-232-25
14	571	92.1	233	4	US-10-858-730-24
15	571	92.1	233	6	US-11-055-822-34
16	571	92.1	233	6	US-11-239-674-52
17	515	92.1	233	6	US-11-116-286-16
18	213	34.4	211	6	US-10-858-730-237
19	170	27.4	199	5	US-10-858-730-93
20	154	24.8	201	5	US-10-858-730-94
21	149	24.0	204	5	US-10-858-730-95
22	140	22.6	203	4	US-10-156-761-8659
23	104	16.8	212	4	US-10-374-903A-6
24	93	15.0	211	4	US-10-282-122A-47826
25	91	14.7	210	4	US-10-335-977-5883
26	91	14.7	210	4	US-10-335-977-5884
27	91	14.7	215	4	US-10-335-977-5885

28	91	14.7	226	4	US-10-425-115-323683	Sequence 323683,
29	91	14.7	252	4	US-10-425-114-65374	Sequence 65374, A
30	89.5	14.4	202	5	US-10-858-730-96	Sequence 96, Appl
31	88.5	14.3	212	6	US-11-136-286-12	Sequence 12, Appl
32	88	14.2	226	3	US-09-738-626-3665	Sequence 3665, Ap
33	85.5	13.8	224	4	US-10-156-761-7796	Sequence 7796, Ap
34	80	12.9	452	6	US-10-096-568A-22692	Sequence 22692, A
35	80	12.9	463	4	US-10-425-115-349872	Sequence 349872,
36	80	12.9	469	4	US-10-425-114-50691	Sequence 50691, A
37	80	12.9	484	6	US-11-096-568A-22691	Sequence 22691, A
38	79.5	12.8	205	3	US-09-927-395-2	Sequence 2, Appl1
39	79.5	12.8	205	3	US-09-847-392-2	Sequence 2, Appl1
40	79.5	12.8	205	6	US-11-106-455-2	Sequence 2, Appl1
41	79.5	12.8	205	6	US-11-091-889-2	Sequence 2, Appl1
42	79.5	12.8	205	6	US-11-091-889-2	Sequence 2, Appl1
43	79.5	12.8	386	5	US-10-954-778-87	Sequence 87, Appl
44	77.5	12.5	195	4	US-10-620-487-2	Sequence 2, Appl1
45	77.5	12.5	195	6	US-11-116-286-14	Sequence 14, Appl

## ALIGNMENTS

```

RESULT 1
US-10-166-142-10
; Sequence 10, Application US/10166142
; Publication No. US20030124687A1
; GENERAL INFORMATION:
; APPLICANT: GUNJI, YOSHIDA
; TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL
; FILE REFERENCE: 223789US
; CURRENT APPLICATION NUMBER: US/10/166,142
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: JP 2001-177075
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Brevibacterium lactofermentum
US-10-166-142-10

Query Match      100.0%; Score 620; DB 4; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.9e-63;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MVMEIFITGILLGASLLSISGPONVLVIKQIGREGIAVLVCLISDVPLFTAGTIGV 60
      |||||
DB      1 MVMEIFITGILLGASLLSISGPONVLVIKQIGREGIAVLVCLISDVPLFTAGTIGV 60
      |||||

QY      61 DLSSNAPVIVDIRMGIAVLLMFAYMAKADMTNKVEAPQIIEETPVPDDTPIGV 120
      |||||
DB      61 DLSSNAPVIVDIRMGIAVLLMFAYMAKADMTNKVEAPQIIEETPVPDDTPIGV 120
      |||||

QY      121 GGGH 124
      |||||
DB      121 GGGH 124
      |||||

RESULT 2
US-10-716-473-10
; Sequence 10, Application US/10716473
; Publication No. US20040142435A1
; GENERAL INFORMATION:
; APPLICANT: Ajinomoto Co. Inc.
; TITLE OF INVENTION: Method for Producing L-Amino Acid Using Methyloctroph
; FILE REFERENCE: 081629
; CURRENT APPLICATION NUMBER: US/10/716,473
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: JP 2002-336346

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PRIOR FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 10  
LENGTH: 124  
TYPE: PRT  
ORGANISM: Brevibacterium lactofermentum  
US-10-716-473-10

Query Match 100.0%; Score 620; DB 4; Length 124;  
Best Local Similarity 100.0%; Pred. No. 1.9e-63;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTMEIFITGLLIGASLLSIGPQNVLVKQIKREGIAVLVCLISDVFLFIAGTLGV 60  
DB 1 MVTMEIFITGLLIGASLLSIGPQNVLVKQIKREGIAVLVCLISDVFLFIAGTLGV 60  
DB 61 DLISNAPIVLDIMRWGIAVILMFVMAAKDAMTNKVEAPQIIETETPTVDDTPIGVF 120  
QY 121 GGCH 124  
DB 121 GGCH 124

RESULT 3  
US-10-784-986-24  
Sequence 24, Application US/10784986  
Publication No. US20040229311A1  
GENERAL INFORMATION:  
APPLICANT: HIRANO, Seiko  
TITLE OF INVENTION: Novel lysine decarboxylase gene and method for  
FILE REFERENCE: US-109  
CURRENT APPLICATION NUMBER: US/10/784,986  
CURRENT FILING DATE: 2004-02-25  
PRIOR APPLICATION NUMBER: JP 2003-47185  
PRIOR FILING DATE: 2003-02-25  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 24  
LENGTH: 124  
TYPE: PRT  
ORGANISM: Brevibacterium lactofermentum  
US-10-784-986-24

Query Match 100.0%; Score 620; DB 5; Length 124;  
Best Local Similarity 100.0%; Pred. No. 1.9e-63;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTMEIFITGLLIGASLLSIGPQNVLVKQIKREGIAVLVCLISDVFLFIAGTLGV 60  
DB 1 MVTMEIFITGLLIGASLLSIGPQNVLVKQIKREGIAVLVCLISDVFLFIAGTLGV 60  
QY 61 DLISNAPIVLDIMRWGIAVILMFVMAAKDAMTNKVEAPQIIETETPTVDDTPIGVF 120  
DB 61 DLISNAPIVLDIMRWGIAVILMFVMAAKDAMTNKVEAPQIIETETPTVDDTPIGVF 120

QY 121 GGCH 124  
DB 121 GGCH 124

RESULT 4  
US-10-716-470-10  
Sequence 10, Application US/10716470  
Publication No. US20050003495A1  
GENERAL INFORMATION:  
APPLICANT: Ajinomoto Co., Inc.  
TITLE OF INVENTION: Method For Producing L-lysine or L-Arginine By Using  
TITLE OF INVENTION: Mechanol Assimilating Bacteria

FILE REFERENCE: OP1628  
CURRENT APPLICATION NUMBER: US/10/716,470  
CURRENT FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: JP 2002-336340  
PRIOR FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 10  
LENGTH: 124  
TYPE: PRT  
ORGANISM: Brevibacterium lactofermentum  
US-10-716-470-10

Query Match 100.0%; Score 620; DB 5; Length 124;  
Best Local Similarity 100.0%; Pred. No. 1.9e-63;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTMEIFITGLLIGASLLSIGPQNVLVKQIKREGIAVLVCLISDVFLFIAGTLGV 60  
DB 1 MVTMEIFITGLLIGASLLSIGPQNVLVKQIKREGIAVLVCLISDVFLFIAGTLGV 60  
DB 61 DLISNAPIVLDIMRWGIAVILMFVMAAKDAMTNKVEAPQIIETETPTVDDTPIGVF 120  
QY 121 GGCH 124  
DB 121 GGCH 124

RESULT 5  
US-09-738-626-6955  
Sequence 6955, Application US/09738626  
Publication No. US20020197605A1  
GENERAL INFORMATION:  
APPLICANT: NAKAGAWA, SATOSHI  
APPLICANT: MIZOGUCHI, HIROSHI  
APPLICANT: ANDO, SEIKO  
APPLICANT: HAYASHI, MIKIRO  
APPLICANT: OCHIAI, KEIKO  
APPLICANT: YOKOI, HARUHIKO  
APPLICANT: TATEISHI, NAOKO  
APPLICANT: SENOH, AKIHIRO  
APPLICANT: IKEDA, MASATO  
APPLICANT: OZAKI, AKIO  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-125  
CURRENT APPLICATION NUMBER: US/09/738,626  
CURRENT FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: JP 99/377484  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: JP 00/159162  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: JP 00/280988  
PRIOR FILING DATE: 2000-08-03  
NUMBER OF SEQ ID NOS: 7059  
SOFTWARE: Patentin ver. 3.0  
SEQ ID NO 6955  
LENGTH: 236  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
US-09-738-626-6955

Query Match 94.2%; Score 584; DB 3; Length 236;  
Best Local Similarity 100.0%; Pred. No. 6.3e-59;  
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTMEIFITGLLIGASLLSIGPQNVLVKQIKREGIAVLVCLISDVFLFIAGTLGV 60  
DB 1 MVTMEIFITGLLIGASLLSIGPQNVLVKQIKREGIAVLVCLISDVFLFIAGTLGV 60  
QY 61 DLISNAPIVLDIMRWGIAVILMFVMAAKDAMTNKVEAPQIIETETPTVDDTPIGV 118

Db 61 DLSNAPIVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETEPTVPDDTPLG 118

RESULT 6  
US-10-166-142-8  
; Sequence 8, Application US/10166142  
; Publication No. US20030124687A1  
; GENERAL INFORMATION:  
; APPLICANT: GUNJI, YOSHIYA  
; APPLICANT: YASUEDA, HISASHI  
; TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE OR L-ARGININE BY USING METHANOL  
; FILE REFERENCE: 223/89US  
; CURRENT APPLICATION NUMBER: US/10/166,142  
; CURRENT FILING DATE: 2002-06-11  
; PRIOR APPLICATION NUMBER: JP 2001-1777075  
; PRIOR FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 3.1  
; SEQ ID NO 8  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Brevibacterium lactofermentum  
US-10-166-142-8

Query Match 94.2%; Score 584; DB 4; Length 236;  
Best Local Similarity 100.0%; Pred. No. 6.3e-59;  
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIMEIFITGILLGASLLSIGPQNVLVIKGIRKREGIAVLVCLISDVFLFIAGTIGV 60  
DB 1 WIMEIFITGILLGASLLSIGPQNVLVIKGIRKREGIAVLVCLISDVFLFIAGTIGV 60

Db 61 DLSNAPIVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETEPTVPDDTPLG 118  
61 DLSNAPIVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETEPTVPDDTPLG 118

RESULT 7  
US-10-716-473-8  
; Sequence 8, Application US/10716473  
; Publication No. US20040142435A1  
; GENERAL INFORMATION:  
; APPLICANT: Ajinomoto Co. Inc.  
; TITLE OF INVENTION: Method for Producing L-Amino Acid Using Methylotroph  
; FILE REFERENCE: OP1629  
; CURRENT APPLICATION NUMBER: US/10/716,473  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: JP 2002-336346  
; PRIOR FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Brevibacterium lactofermentum  
US-10-716-473-8

Query Match 94.2%; Score 584; DB 4; Length 236;  
Best Local Similarity 100.0%; Pred. No. 6.3e-59;  
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIMEIFITGILLGASLLSIGPQNVLVIKGIRKREGIAVLVCLISDVFLFIAGTIGV 60  
DB 1 WIMEIFITGILLGASLLSIGPQNVLVIKGIRKREGIAVLVCLISDVFLFIAGTIGV 60

QY 61 DLSNAPIVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETEPTVPDDTPLG 118  
61 DLSNAPIVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETEPTVPDDTPLG 118

RESULT 8  
US-10-716-480A-2

; Sequence 2, Application US/10716480A  
; Publication No. US20040146974A1  
; GENERAL INFORMATION:  
; APPLICANT: Ajinomoto Co. Inc.  
; TITLE OF INVENTION: Method for Producing L-Amino Acid Using Methylotroph  
; FILE REFERENCE: OP1627/US-102  
; CURRENT APPLICATION NUMBER: US/10/716,480A  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: JP 2002-336315  
; PRIOR FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Brevibacterium lactofermentum  
US-10-716-480A-2

Query Match 94.2%; Score 584; DB 4; Length 236;  
Best Local Similarity 100.0%; Pred. No. 6.3e-59;  
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIMEIFITGILLGASLLSIGPQNVLVIKGIRKREGIAVLVCLISDVFLFIAGTIGV 60  
DB 1 WIMEIFITGILLGASLLSIGPQNVLVIKGIRKREGIAVLVCLISDVFLFIAGTIGV 60

QY 61 DLSNAPIVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETEPTVPDDTPLG 118  
61 DLSNAPIVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETEPTVPDDTPLG 118

RESULT 9  
US-10-760-283-18  
; Sequence 18, Application US/10760283  
; Publication No. US20040214296A1  
; GENERAL INFORMATION:  
; APPLICANT: ASAHARA, Takayuki  
; APPLICANT: HIRANO, Seiko  
; APPLICANT: YASUEDA, Hisashi  
; TITLE OF INVENTION: Method for Producing L-Lysine Using Methanol-utilizing Bacterium  
; FILE REFERENCE: OP1631  
; CURRENT APPLICATION NUMBER: US/10/760,283  
; CURRENT FILING DATE: 2004-01-21  
; PRIOR APPLICATION NUMBER: JP 2003-20513  
; PRIOR FILING DATE: 2003-01-29  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Brevibacterium lactofermentum  
US-10-760-283-18

Query Match 94.2%; Score 584; DB 4; Length 236;  
Best Local Similarity 100.0%; Pred. No. 6.3e-59;  
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WIMEIFITGILLGASLLSIGPQNVLVIKGIRKREGIAVLVCLISDVFLFIAGTIGV 60  
DB 1 WIMEIFITGILLGASLLSIGPQNVLVIKGIRKREGIAVLVCLISDVFLFIAGTIGV 60

QY 61 DLSNAPIVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETEPTVPDDTPLG 118  
61 DLSNAPIVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETEPTVPDDTPLG 118

RESULT 10  
US-10-784-986-22  
; Sequence 22, Application US/10784986  
; Publication No. US20040229311A1  
; GENERAL INFORMATION:  
; APPLICANT: HIRANO, Seiko  
; APPLICANT: YASUEDA, Hisashi

```

; TITLE OF INVENTION: Novel lysine decarboxylase gene and method for
; FILE REFERENCE: US-109
; CURRENT APPLICATION NUMBER: US/10/784,986
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: JP 2003-47185
; PRIOR FILING DATE: 2003-02-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 22
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Brevibacterium lactofermentum
US-10-784-986-22

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Query Match          94.2%; Score 584; DB 5; Length 236;
Best Local Similarity 100.0%; Pred. No. 6.3e-59;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MVTMEFITGLLGASLLSIGPQNVIVIKGIRREGIIVLVCLISDVFLFIAGTGLGV 60
DB 1 MVTMEFITGLLGASLLSIGPQNVIVIKGIRREGIIVLVCLISDVFLFIAGTGLGV 60
61 DLSNAPIVLDIRMGIGIAYLLMFVMAAKDAMTNKVEAPQIIEETPTVPDDTPLG 118
61 DLSNAPIVLDIRMGIGIAYLLMFVMAAKDAMTNKVEAPQIIEETPTVPDDTPLG 118

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RESULT 11
US-10-716-470-8
; Sequence 8, Application US/10716470
; Publication No. US20050003495A1
; GENERAL INFORMATION:
; APPLICANT: Ajinomoto Co. Inc.
; TITLE OF INVENTION: Method For Producing L-lysine or L-Arginine By Using
; FILE REFERENCE: OP1628
; CURRENT APPLICATION NUMBER: US/10/716,470
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: JP 2002-336340
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Brevibacterium lactofermentum
US-10-716-470-8

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Query Match          94.2%; Score 584; DB 5; Length 236;
Best Local Similarity 100.0%; Pred. No. 6.3e-59;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 MVTMEFITGLLGASLLSIGPQNVIVIKGIRREGIIVLVCLISDVFLFIAGTGLGV 60
DB 1 MVTMEFITGLLGASLLSIGPQNVIVIKGIRREGIIVLVCLISDVFLFIAGTGLGV 60
61 DLSNAPIVLDIRMGIGIAYLLMFVMAAKDAMTNKVEAPQIIEETPTVPDDTPLG 118
61 DLSNAPIVLDIRMGIGIAYLLMFVMAAKDAMTNKVEAPQIIEETPTVPDDTPLG 118

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RESULT 12
US-09-746-660A-52
; Sequence 52, Application US/09746660A
; Publication No. US20030049804A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Krieger, Burkhard
; APPLICANT: Schröder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberer, Gregor
; APPLICANT: Klm, Jun-Mon

```

```

; APPLICANT: Lee, Heung-Schick
; APPLICANT: Hang, Byung-Joon
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CP2
; CURRENT APPLICATION NUMBER: US/09/746,660A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/606740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 09/603124
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: Patentin Vers. 2.0
; SEQ ID NO 52
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-746-660A-52

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Query Match          92.1%; Score 571; DB 3; Length 233;
Best Local Similarity 100.0%; Pred. No. 2e-57;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 MEIFITGLLGASLLSIGPQNVIVIKGIRREGIIVLVCLISDVFLFIAGTGLVDLL 63
DB 1 MEIFITGLLGASLLSIGPQNVIVIKGIRREGIIVLVCLISDVFLFIAGTGLVDLL 60
64 SNAPIVLDIRMGIGIAYLLMFVMAAKDAMTNKVEAPQIIEETPTVPDDTPLG 118
61 SNAPIVLDIRMGIGIAYLLMFVMAAKDAMTNKVEAPQIIEETPTVPDDTPLG 115

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RESULT 13
US-10-196-232-25
; Sequence 25, Application US/10196232
; Publication No. US20030113899A1
; GENERAL INFORMATION:
; APPLICANT: YAMAGUCHI, MIKIKO
; APPLICANT: ITO, HISAO
; APPLICANT: GUNJI, YOSHIA
; APPLICANT: YASUEDA, HISASHI
; TITLE OF INVENTION: METHOD FOR PRODUCING L-ARGININE
; FILE REFERENCE: 225391US0
; CURRENT APPLICATION NUMBER: US/10/196,232
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: JP 2001-224586
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 25
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-196-232-25

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Query Match          92.1%; Score 571; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 2e-57;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 MEIFITGLLGASLLSIGPQNVIVIKGIRREGIIVLVCLISDVFLFIAGTGLVDLL 63
DB 1 MEIFITGLLGASLLSIGPQNVIVIKGIRREGIIVLVCLISDVFLFIAGTGLVDLL 60

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OY 64 SNAAPVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETETPTVPDDTPLG 118  
 DB 61 SNAAPVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETETPTVPDDTPLG 115

# RESULT 14

US-10-858-730-234  
 ; Sequence 234, Application US/10858730  
 ; Publication No. US20050255568A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bailey, Richard B.  
 ; APPLICANT: Blomquist, Paul  
 ; APPLICANT: Doten, Reed  
 ; APPLICANT: Driggers, Edward M.  
 ; APPLICANT: Madden, Kevin T.  
 ; APPLICANT: O'Leary, Jessica  
 ; APPLICANT: O'Toole, George  
 ; APPLICANT: Trueheart, Joshua  
 ; APPLICANT: Walbridge, Michael J.  
 ; APPLICANT: Yorgey, Peter S.  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID  
 ; FILE OF INVENTION: PRODUCTION  
 ; FILE REFERENCE: 14184-030001  
 ; CURRENT APPLICATION NUMBER: US/10/858,730  
 ; CURRENT FILING DATE: 2004-06-01  
 ; PRIOR APPLICATION NUMBER: US 60/475,000  
 ; PRIOR FILING DATE: 2003-05-30  
 ; PRIOR APPLICATION NUMBER: US 60/551,860  
 ; PRIOR FILING DATE: 2004-03-10  
 ; NUMBER OF SEQ ID NOS: 364  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 234  
 ; LENGTH: 233  
 ; TYPE: PRT  
 ; ORGANISM: Coryne-bacterium glutamicum  
 ; US-10-858-730-234

Query Match 92.1%; Score 571; DB 5; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 2e-57;  
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MEIFITGLLGASLSLISIPQNVLVTKQIKREGIAVLLVCLISDVFLFIAGTLGVDLL 63  
 DB 1 MEIFITGLLGASLSLISIPQNVLVTKQIKREGIAVLLVCLISDVFLFIAGTLGVDLL 60  
 OY 64 SNAAPVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETETPTVPDDTPLG 118  
 DB 61 SNAAPVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETETPTVPDDTPLG 115

# RESULT 15

US-11-055-822-54  
 ; Sequence 54, Application US/11055822  
 ; Publication No. US20050260707A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pompeius, Markus  
 ; APPLICANT: Kroger, Burkhard  
 ; APPLICANT: Schroder, Hartwig  
 ; APPLICANT: Zelder, Oskar  
 ; APPLICANT: Haberer, Gregor  
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
 ; FILE OF INVENTION: METABOLIC PATHWAY PROTEINS  
 ; FILE REFERENCE: BGI-121PCN  
 ; CURRENT APPLICATION NUMBER: US/11/055,822  
 ; CURRENT FILING DATE: 2005-02-11  
 ; PRIOR APPLICATION NUMBER: 09/606,740  
 ; PRIOR FILING DATE: 2000-06-23  
 ; PRIOR APPLICATION NUMBER: 60/141,031  
 ; PRIOR FILING DATE: 1999-06-25  
 ; PRIOR APPLICATION NUMBER: 60/142,101  
 ; PRIOR FILING DATE: 1999-07-02  
 ; PRIOR APPLICATION NUMBER: 60/148,613  
 ; PRIOR FILING DATE: 1999-08-12

; PRIOR APPLICATION NUMBER: 60/187,970  
 ; PRIOR FILING DATE: 2000-03-09  
 ; PRIOR APPLICATION NUMBER: DE 19930476.9  
 ; PRIOR FILING DATE: 1999-07-01  
 ; PRIOR APPLICATION NUMBER: DE 19931415.2  
 ; PRIOR FILING DATE: 1999-07-08  
 ; PRIOR APPLICATION NUMBER: DE 19931418.7  
 ; PRIOR FILING DATE: 1999-07-08  
 ; PRIOR APPLICATION NUMBER: DE 19931419.5  
 ; PRIOR FILING DATE: 1999-07-08  
 ; PRIOR APPLICATION NUMBER: DE 19931420.9  
 ; PRIOR FILING DATE: 1999-07-08  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 1158  
 ; SEQ ID NO 54  
 ; LENGTH: 233  
 ; TYPE: PRT  
 ; ORGANISM: Corynebacterium glutamicum  
 ; US-11-055-822-54

Query Match 92.1%; Score 571; DB 6; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 2e-57;  
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MEIFITGLLGASLSLISIPQNVLVTKQIKREGIAVLLVCLISDVFLFIAGTLGVDLL 63  
 DB 1 MEIFITGLLGASLSLISIPQNVLVTKQIKREGIAVLLVCLISDVFLFIAGTLGVDLL 60  
 OY 64 SNAAPVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETETPTVPDDTPLG 118  
 DB 61 SNAAPVLDIMRWGIAVLLMFVMAAKDAMTNKVEAPQIIETETPTVPDDTPLG 115

Search completed: July 19, 2006, 00:46:18  
 Job time : 189 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 19, 2006, 00:25:46 ; Search time 40 Seconds

(without alignments)  
298.272 Million cell updates/sec

Title: US-10-716-470-10

Perfect score: 620

Sequence: 1 MVIMEIFITGLLIGASLLS.....EETEPVDPDPLGFCGGH 124

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	213	34.4	211	1	OQEC5A
2	210	33.9	211	2	E85948
3	210	33.9	211	2	B91103
4	205	33.1	211	2	AH0874
5	199.5	32.2	205	2	AG0112
6	193.5	31.2	202	2	C97472
7	193.5	31.2	202	2	AG2690
8	172.5	27.8	200	2	D83100
9	170	27.4	199	2	H70756
10	169	27.3	204	2	AD3411
11	154	24.8	201	2	C70744
12	135	21.8	211	2	S57940
13	116	18.7	211	2	B82318
14	109	17.6	210	2	D84016
15	107	17.3	210	2	E87252
16	105	16.9	220	2	D69638
17	104	16.8	205	2	B89854
18	99	16.0	212	2	AD0714
19	94.5	15.2	235	2	AD2904
20	94.5	15.2	235	2	F97679
21	94	15.2	216	2	AH3203
22	92	14.8	200	2	G83703
23	91	14.7	208	2	G84086
24	91	14.7	210	2	F64609
25	91	14.7	210	2	B71906
26	88.5	14.3	212	2	F64940
27	87	14.0	195	2	AF0830
28	86	13.9	197	2	B83280
29	86	13.9	207	2	E83703

30	86	13.9	213	2	F83444	hypothetical prote
31	85.5	13.8	222	2	F82353	conserved hypochet
32	84.5	13.6	209	2	E82388	conserved hypochet
33	84	13.5	210	2	AC2282	RhtB family transp
34	83.5	13.5	278	2	E98301	hypothetical prote
35	82.5	13.5	218	2	A96009	probable amino aci
36	82.5	13.3	212	2	G80942	hypothetical prote
37	82.5	13.3	212	2	G85790	hypothetical prote
38	82.5	13.3	213	2	E97789	hypothetical prote
39	80	12.9	208	1	B69066	conserved hypochet
40	80	12.9	343	2	G87419	cytochrome c oxida
41	80	12.9	510	2	G71365	probable carnitine
42	79.5	12.8	210	2	G83082	hypothetical prote
43	79.5	12.8	442	2	T24196	hypothetical prote
44	79	12.7	222	2	E87264	efflux protein, Ly
45	78	12.6	212	2	AB3270	threonine efflux p

## ALIGNMENTS

## RESULT 1

OQEC5A  
hypothetical 23k protein (sbm-fba intergenic region) - Escherichia coli (strain K-12)

C/Species: Escherichia coli

C/Date: 31-Dec-1990 #sequence\_revision 17-Oct-1997 #text\_change 09-Jul-2004

C/Accession: B65077; S04736

R/Blatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; (

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A/Title: The complete genome sequence of Escherichia coli K-12.

A/Reference number: A64720, MWID:97426617, PMID:9278503.

A/Accession: B65077

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-211 <BLAT>

A/Cross-references: UNIPROT:P11667; UNIPARC:UPI000033982; GB:AE000375; GB:U00096; NID:

A/Experimental source: strain K-12, substrain MG1655

R/Alfunder, P.R.; Perham, R.N.

Mol. Microbiol. 3, 723-732, 1989

A/Title: Identification, molecular cloning and sequence analysis of a gene cluster enc

hyde 3-phosphate dehydrogenase of Escherichia coli.

A/Reference number: S04730, MWID:89313302, PMID:2546007

A/Accession: S04736

A/Molecule type: DNA

A/Residues: 15-211 <ALP>

A/Cross-references: UNIPARC:UPI000016130; EMBL:X14436; NID:941417; PIDN:CAA32607.1; P1

C/Genetics:

A/Gene: Y9GA

A/Map position: 63 min

C/Superfamily: Escherichia coli hypothetical 23k protein (sbm-fba intergenic region)

## Query Match

Best Local Similarity 34.4%; Score 213; DB 1; Length 211;

Matches 40; Conservative 21; Mismatches 32; Indels 0; Gaps 0;

## QY

7 FITGLIGASLLSISGPQVAVITKQIKREGIIVLVCLISDVFLFNGTIGVLLSNA 66

5 YFQGLALGAMTLLPSPQAFVFNQGIIRQYHIMALLCAISDLVICGIRGGSALLMQ 64

## DB

67 APIVDIMRMGIAVLTFWVAAMADMTNKVE 99

65 SPMLALVTVGVAFLTWGFGAFRTANSSNE 97

## QY

## RESULT 2

## E85948

hypothetical protein Y9GA [imported] - Escherichia coli (strain O157:H7, substrain EDJ9

C/Species: Escherichia coli

C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

C/Accession: E85948

R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayne

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamoustis, K.; Apodaca

C:\Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002

C:\Accession: AH0874

R:\Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:\Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A:\Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar

A:\Reference number: AB0502; MUID:21534947; PMID:11577608

A:\Accession: AH0874

A:\Status: preliminary

A:\Molecule type: DNA

A:\Residues: 1-211 <PAR>

A:\Cross-references: UNIPARC:UP1000005A426; GB:AL513382; PIDD:CAD002896.1; PID:916504149; C:\Genetics:

A:\Gene: STY3222

C:\Superfamily: Escherichia coli hypothetical 23k protein (sbm-fba intergenic region)

Query Match 33.1%; Score 205; DB 2; Length 211;

Best Local Similarity 38.1%; Pred. No. 4e-13;

Matches 37; Conservative 26; Mismatches 34; Indels 0; Gaps 0;

Oy 3 IMEFTIGLLGASLLSIGPONVLYIKGIREGLIAYLVLCISDVFLFIAGTVGL 62

Db 1 MISYFGVALGAMIRPLGPONAFVNNQGIKRRQYHMLIALCALSDVLISAGIFGSA 60

Oy 63 LSNAAPVLDIMRWGIAVLLMPFAVMAKDAKMTKVE 99

Db 61 LMQSPWLLALVTWGVAFLLWYGFGLKXTAMSSNLE 97

RESULT 5

AG0112

Probable lysE type translocator YP00918 [imported] - Yersinia pestis (strain CO92)

C:\Species: Yersinia pestis

C:\Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004

C:\Accession: AG0112

R:\Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tildall, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Marras, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Ill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, Nature 413, 523-527, 2001

A:\Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:\Reference number: AB0001; MUID:21470413; PMID:11586360

A:\Accession: AG0112

A:\Status: preliminary

A:\Molecule type: DNA

A:\Residues: 1-205 <KUR>

A:\Cross-references: UNIPROT:Q8ZHH6; UNIPARC:UP100000DC792; GB:AL590842; PIDD:CA089762.1; C:\Genetics:

A:\Gene: YP00918

C:\Superfamily: Escherichia coli hypothetical 23k protein (sbm-fba intergenic region)

Query Match 32.2%; Score 199.5; DB 2; Length 205;

Best Local Similarity 38.5%; Pred. No. 1.4e-12;

Matches 35; Conservative 27; Mismatches 26; Indels 3; Gaps 1;

Oy 3 IMEFTIGLLGASLLSIGPONVLYIKGIREGLIAYLVLCISDVFLFIAGTVGL 62

Db 1 MLNAVYLGHFILASAMIRPLGPONVFNQGIKRRQYHMLIALCALSDIILICAGIFGSA 60

Oy 63 LSNAAPVLDIMRWGIAVLLMPFAVMAKDAKMTKVE 99

Db 61 LLSKSPVLLALVTWGVAFLLWYGFGLKXTAMSSNLE 91

RESULT 6

C97472

Probable membrane transport protein. (AL537613) [imported] - Agrobacterium tumefaciens (

C:\Species: Agrobacterium tumefaciens

C:\Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004

C:\Accession: C97472

A:\Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;



A:Accession: AD3411  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-204 <KOR>  
 A:Cross-references: UNIPROT:Q8YG87; UNIPARC:UPI0000057EE3; GB:AE008917; PIDN:AAL52455.1;  
 A:Experimental source: strain 16M  
 C:Genetics:  
 A:Gene: BMEL1274  
 A:Map position: 1  
 C:Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)

Query Match 27.3%; Score 169; DB 2; Length 204;  
 Best Local Similarity 35.4%; Pred. No. 1.5e-09;  
 Matches 34; Conservative 24; Mismatches 36; Indels 2; Gaps 1;

QY 8 ITGLLGASLLSTGPONLVIKGIRKREGIAVLVCLISDVFLFIAGTGVLDLSNAA 67  
 Db 6 LSGFLGASLLIAIGAGAFILROGLRQHFILCLISDALISAGVAGLTLAQS 65  
 QY 68 PIVLDIRMGIAVLWFAVMAAKDAMTKVEAPQI 103  
 Db 66 PKLIAFVTLGAAFLFWYASVAFRRAF--HPEAMOV 99

RESULT 11  
 C70744  
 hypothetical protein Rv0488 - Mycobacterium tuberculosis (strain H37RV)  
 C:Species: Mycobacterium tuberculosis  
 C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
 C:Accession: C70744  
 R:Coile, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998  
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.  
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A:Reference number: A70500; MUID:98295987; PMID:9631230  
 A:Accession: C70744  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-201 <COL>  
 A:Cross-references: UNIPROT:Q1154; UNIPARC:UPI0000139897; GB:Z77162; GB:AL123456; NID:5  
 A:Experimental source: strain H37RV  
 C:Genetics:  
 A:Gene: Rv0488  
 C:Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)

Query Match 24.8%; Score 154; DB 2; Length 201;  
 Best Local Similarity 39.7%; Pred. No. 4.6e-08;  
 Matches 31; Conservative 23; Mismatches 24; Indels 0; Gaps 0;

QY 16 SLLSTGPONLVIKGIRKREGIAVLVCLISDVFLFIAGTGVLDLSNAAPIVLDIMR 75  
 Db 3 TLKRAIPQNAFVIRQGIIRREYLVIVALCGIADGALIAVGGFALIHHPMTLVAR 62  
 QY 76 WGGIAYLLMFVMAAKDA 93  
 Db 63 FCGAFLIGYALLAAKVA 80

RESULT 12  
 S57940  
 YggA protein homolog - Aeromonas hydrophila  
 C:Species: Aeromonas hydrophila  
 C>Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 08-Oct-1999  
 C:Accession: S57940  
 R:Swift, S.; Fish, L.; Williams, P.; Stewart, G.S.A.B.  
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and submitted to the EMBL Data Library, July 1995  
 A:Reference number: S57938  
 A:Accession: S57940  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-211 <SMI>

A:Cross-references: UNIPARC:UPI000016E4DC; EMBL:X89469; NID:g899143; PIDN:CA61655.1; P:  
 Query Match 21.8%; Score 135; DB 2; Length 211;  
 Best Local Similarity 29.3%; Pred. No. 3.8e-06;  
 Matches 27; Conservative 22; Mismatches 39; Indels 4; Gaps 1;

QY 17 LLSIGPONLVIKGIRKREGIAVLVCLISDVFLFIAGTGVLDLSNAAPIVLDIMRW 76  
 Db 1 MIIPIGQNAFVLSRGIRHRRHLLITATLCLCDLVIGIVGAGNLLASPIGLALLTW 60  
 QY 77 GGIAYLLMFVMAAKDAMTK---VEAPQII 104  
 Db 61 GGVILGCMFGRISLSAARGAKLADSPQLM 92

RESULT 13  
 B82318  
 Lyse/YggA family protein VC0481 [imported] - Vibrio cholerae (strain N16961 serogroup O:  
 C:Species: Vibrio cholerae  
 C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
 C:Accession: B82318  
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, J. 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
 A:Reference number: A82035; MUID:20406833; PMID:10952301  
 A:Accession: B82318  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-211 <HEI>  
 A:Cross-references: UNIPROT:Q9KDM4; UNIPARC:UPI00000C2CE3; GB:AE004134; GB:AE003852; NII  
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
 C:Genetics:  
 A:Gene: VC0481  
 A:Map position: 1  
 C:Superfamily: Escherichia coli hypothetical 23K protein (sbm-fba intergenic region)

Query Match 18.7%; Score 116; DB 2; Length 211;  
 Best Local Similarity 26.7%; Pred. No. 0.0003;  
 Matches 31; Conservative 21; Mismatches 60; Indels 4; Gaps 1;

QY 6 IFITGLLAGSLLSTGPONLVIKGIRKREGIAVLVCLISDVFLFIAGTGVLDLSN 65  
 Db 5 ILLGFSLGATMIIPGQNAFVLSRGIRHRRHLLITATTCGVDIMFITIGTGGGLIS 64  
 QY 66 AAPIVDIRMGIAVLWFAVMAAKDAMTKVEAPQIIEETEPVDDTPIGVP 121  
 Db 65 QNTSLIIGVTLGILFLFCGFGFLSLRAL---KPDQASSTANPMAGRAKAVIFG 116

RESULT 14  
 D84016  
 hypothetical protein BH2932 [imported] - Bacillus halodurans (strain C-125)  
 C:Species: Bacillus halodurans  
 C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
 C:Accession: D84016  
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai  
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A:Reference number: A83650; MUID:20512582; PMID:11058132  
 A:Accession: D84016  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-210 <STO>  
 A:Cross-references: UNIPROT:Q9K8S1; UNIPARC:UPI00000C4058; GB:AP001517; GB:BA000004; NII  
 A:Experimental source: strain C-125  
 C:Genetics:  
 A:Gene: BH2932  
 C:Superfamily: hypothetical protein b1798

Query Match 17.6%; Score 109; DB 2; Length 210;  
 Best Local Similarity 32.1%; Pred. No. 0.0015;



## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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OM protein - protein search, using sw model

Run on: July 19, 2006, 00:22:17 / Search time 298 Seconds

(without alignments)  
384.906 Million cell updates/sec

Title: US-10-716-470-10

Perfect score: 620  
Sequence: 1 MWIMEIFITGLLGASLLS.....EETEPVDDPTPLGVGGG 124

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database: Uniprot\_7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_tramb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	607	97.9	121	2 Q4H475_CORGL	Q4H475 corynebacte
2	571	92.1	233	1 LYSE_CORGL	P94633 corynebacte
3	571	92.1	233	2 Q4H476_CORGL	Q4H476 corynebacte
4	389.5	62.8	228	1 LYSE_CORGL	Q4H476 corynebacte
5	271	43.7	228	1 LYSE_CORGL	Q4H476 corynebacte
6	214	34.5	211	1 ARGO_ECOLI	Q4H476 corynebacte
7	214	34.5	211	1 Q32BY3_SHIDS	Q4H476 corynebacte
8	213	34.4	211	1 ARGO_ECOLI	Q4H476 corynebacte
9	213	34.4	211	1 Q2M9R9_ECOLI	Q4H476 corynebacte
10	212	34.2	211	1 Q3YXU9_SHISS	Q4H476 corynebacte
11	210	33.9	211	1 ARGO_ECOLI	Q4H476 corynebacte
12	210	33.9	211	1 ARGO_SHIFL	Q4H476 corynebacte
13	207	33.4	211	1 Q3IWT2_SHIBS	Q4H476 corynebacte
14	205	33.1	211	1 ARGO_SALTI	Q4H476 corynebacte
15	204	32.9	211	1 ARGO_SALCH	Q4H476 corynebacte
16	204	32.9	211	1 ARGO_SALTY	Q4H476 corynebacte
17	200	32.3	211	1 ARGO_SALPA	Q4H476 corynebacte
18	199.5	32.2	205	1 ARGO_YERPE	Q4H476 corynebacte
19	199.5	32.2	205	1 ARGO_YERPE	Q4H476 corynebacte
20	198	31.9	204	1 ARGO_YERPE	Q4H476 corynebacte
21	194	31.9	204	1 ARGO_YERPE	Q4H476 corynebacte
22	193.5	31.2	202	2 Q5LUM5_SILPO	Q4H476 corynebacte
23	191.5	30.9	196	2 Q4NL65_GMTCC	Q4H476 corynebacte
24	189	30.5	200	2 Q3H1Y4_GACTO	Q4H476 corynebacte
25	189	30.5	202	2 Q2K7B0_RHRET	Q4H476 corynebacte
26	187.5	30.2	203	2 Q4O6B0_YRHOE	Q4H476 corynebacte
27	187	30.2	200	2 Q4ZP34_PSEU2	Q4H476 corynebacte
28	186	30.0	221	2 Q4OYM9_KINRA	Q4H476 corynebacte
29	185	29.8	203	2 Q2RMA4_RHORB	Q4H476 corynebacte
30	183	29.5	200	2 Q48EJ3_PSE14	Q4H476 corynebacte
31	183	29.5	206	2 Q7ZE15_DESVH	Q4H476 corynebacte

## ALIGNMENTS

32	180	29.0	200	2	Q87X28_PSESM	Q87X28 pseudomonas
33	179	28.9	202	2	Q8XXT9_RALSO	Q8XXT9 ralsconia s
34	178	28.7	214	2	Q39T4_BURB3	Q39T4 burkholderi
35	177	28.5	212	2	Q8Y2F1_RALSO	Q8Y2F1 ralsconia s
36	176	28.4	207	1	ARGO_PFOUL	Q7N183 photorhabdu
37	175	28.2	200	2	Q4K777_PSEPS	Q4K777 pseudomonas
38	174	28.1	204	2	Q227Y0_9GAMM	Q227Y0 shewanella
39	174	28.1	204	2	Q35S87_9GAMM	Q35S87 shewanella
40	174	28.1	204	2	Q36DP7_9GAMM	Q36DP7 shewanella
41	174	28.1	211	2	Q7NRY0_CHRYO	Q7NRY0 chromobacte
42	173	27.9	213	2	Q2X624_9GAMM	Q2X624 shewanella
43	173	27.9	213	2	Q2ZLZ4_SHEPU	Q2ZLZ4 shewanella
44	172.5	27.8	200	2	Q9HW36_PSESE	Q9HW36 pseudomonas
45	172	27.7	199	2	Q3PH95_PARDE	Q3PH95 paracoccus

## RESULT 1

Q4H475\_CORGL PRELIMINARY; PRT; 121 AA.

AC Q4H475; 30-AUG-2005, integrated into UniProtKB/TrEMBL.

DT 30-AUG-2005, sequence version 1.

DT 07-FEB-2006, entry version 2.

DE Mutant lysine exporter protein.

GN Name=Lyse24;

OS Corynebacterium glutamicum (Brevibacterium flavum).

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.

OX NCBI\_Taxid=1718;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 13639;

RA Guntl Y., Sugimoto S., Yasuda H.;

RT "Functional expression of mutant lyse gene for production of L-lysine

in Methylophilus methylotrophus.";

RL Submitted (JAN-2005) to the EMBL/Genbank/DBJ databases.

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CC EMBL; AB199585; BAE07189.1; -; Genomic DNA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005293; P:lysine permease activity; IEA.

DR GO; GO:0006865; P:amino acid transport; IEA.

DR InterPro; IPR001123; LyseB.

DR Pfam; PF01810; LyseB; 1.

SEQUENCE 121 AA; 12844 MW; 379986812602DA60 CRC64;

Query Match 97.9%; Score 607; DB 2; Length 121;

Best Local Similarity 100.0%; Pred. No. 6.2e-50; Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	4	MEIFITGLLGASLLSIGPQNVLYIKQIKREGIAVLVCLDVDFLFGTIGVDLL	63
DB	1	MEIFITGLLGASLLSIGPQNVLYIKQIKREGIAVLVCLDVDFLFGTIGVDLL	60
QY	64	SNAPDIVDINRWGIAVLVFAVMAADMTNKVEAPQIIEETPTVDDPTPLGVGGG	123
DB	61	SNAPDIVDINRWGIAVLVFAVMAADMTNKVEAPQIIEETPTVDDPTPLGVGGG	120
QY	124	H 124	
DB	121	H 121	

## RESULT 2

LYSE\_CORGL STANDARD; PRT; 233 AA.

ID P94633; 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.

DT 14-AUG-2001, sequence version 2.  
 DT 07-MAR-2006, entry version 38.  
 DE lysine exporter protein.  
 GN Name=lysE; OrderedLocustNames=Cg11262, cg1424;  
 OS Corynebacterium glutamicum (Brevibacterium flavum).  
 OC Bacteria; Actinobacteria; Actinobacteriales;  
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.  
 NCBI\_TaxID=1718;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND FUNCTION.  
 RC STRAIN=RI27;  
 RX MEDLINE=97126810; PubMed=8971704;  
 RA Vrijic M.M., Sahn H., Eggeling L.;  
 RT "A new type of transporter with a new type of cellular function: L-lysine export from Corynebacterium glutamicum.";  
 RL Mol. Microbiol. 22:815-826(1998).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;  
 RA Nakagawa S.;  
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";  
 RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;  
 RX MEDLINE=22830012; PubMed=1294626; DOI=10.1016/S0168-1656(03)00154-8;  
 RA Kalinowski J., Bathe B., Bartels D., Bischoff N., Bort M., Burkowski A., Duesch N., Eggeling L., Eikmanns B.J., Gaigalat L., Goessens A., Hartmann M., Hutmacher K., Kraemer R., Linke B., McHardy A.C., Meyer F., Moeckel B., Pfeifferle W., Puelhner A., Ray D.A., Rueckert C., Rupp O., Sahn H., Wendisch V.F., Wiegand I., Tauch A.;  
 RT "The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins.";  
 RL J. Biotechnol. 104:5-25(2003).  
 CC -1- FUNCTION: Involved in the efflux of excess of L-lysine. This is necessary to control the intracellular L-lysine level.  
 CC -1- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass membrane protein.  
 CC -1- SIMILARITY: Belongs to the lysE/argo transporter (TC 2.A.75) family.  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
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 CC EMBL, X96471; CA63324.2; -; Genomic DNA.  
 CC EMBL, BA000036; BAB98655.1; ALT\_INIT; Genomic DNA.  
 CC EMBL, BX927151; CAP19965.1; -; Genomic DNA.  
 CC GenomeReviews: BX927147 GR; cg1424.  
 CC GenomeReviews: BA000036 GR; cg11262.  
 CC InterPro: IPR004777; Lys\_exporter.  
 CC InterPro: IPR001123; LysE.  
 CC Pfam: PF01810; LysE; 1.  
 CC TIGRFAMs: TIGR00948; 2a75; 1.  
 CC Complete proteome; Inner membrane; Transmembrane; Transport.  
 CC CHAIN 1 233  
 FT TRANSMEM 3 23  
 FT TRANSMEM 35 55  
 FT TRANSMEM 66 86  
 FT TRANSMEM 144 164  
 FT TRANSMEM 177 197  
 FT TRANSMEM 213 233  
 FT SEQUENCE 233 AA; 25082 MW; FSPD9B1ACAD11D3 CRC64;  
 Query Match 92.1%; Score 571; DB 1; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-46;  
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 SNAPIVLDIRMGIAVLIMFAVMAKADMTNKVEAPQIIETPTVPDDTFLG 118  
 DB 61 SNAPIVLDIRMGIAVLIMFAVMAKADMTNKVEAPQIIETPTVPDDTFLG 115  
 RESULT 3  
 ID Q4H476 CORGL PRELIMINARY; PRT; 233 AA.  
 AC Q4H476 CORGL  
 DT 30-AUG-2005, integrated into UniProtKB/TrEMBL.  
 DT 30-AUG-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 2.  
 DE lysine exporter protein.  
 GN Name=lysE;  
 OS Corynebacterium glutamicum (Brevibacterium flavum).  
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;  
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.  
 NCBI\_TaxID=1718;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ATCC 13869;  
 RA Gunji Y., Sugimoto S., Yasueda H.;  
 RT "Functional expression of mutant lysE gene for production of L-lysine in *Methylophilus methylotrophus*.";  
 RL Submitted (JAN-2005) to the EMBL/Genbank/DBJ databases.  
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 CC EMBL, AB19584; BA07188.1; -; Genomic DNA.  
 CC GO: GO:0016021; C:integral to membrane; IEA.  
 CC GO: GO:0016020; C:membrane; IEA.  
 CC GO: GO:0005293; F:lysine permease activity; IEA.  
 CC GO: GO:0006865; P:amino acid transport; IEA.  
 CC InterPro: IPR004777; Lys\_exporter.  
 CC InterPro: IPR001123; LysE.  
 CC Pfam: PF01810; LysE; 1.  
 CC TIGRFAMs: TIGR00948; 2a75; 1.  
 CC SEQUENCE 233 AA; 25082 MW; FSPD9B1ACAD11D3 CRC64;  
 Query Match 92.1%; Score 571; DB 2; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-46;  
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 SNAPIVLDIRMGIAVLIMFAVMAKADMTNKVEAPQIIETPTVPDDTFLG 118  
 DB 61 SNAPIVLDIRMGIAVLIMFAVMAKADMTNKVEAPQIIETPTVPDDTFLG 115  
 RESULT 4  
 ID LYS\_E COREF STANDARD; PRT; 228 AA.  
 AC Q8RMT4;  
 DT 01-NOV-2002, integrated into UniProtKB/Swiss-Prot.  
 DT 01-NOV-2002, sequence version 2.  
 DT 07-MAR-2006, entry version 24.  
 DE lysine exporter protein.  
 GN Name=lysE; OrderedLocustNames=CE1357;  
 OS Corynebacterium efficiens.  
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;  
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.  
 NCBI\_TaxID=152794;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;  
 RA Iwata H., Kimura E., Kawahara Y., Sugimoto S.;  
 RT "lysE, lysE of Corynebacterium efficiens.";  
 RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.

(2)  
 RN NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).  
 RP STRAIN=YS-314 / AJ12310 / DSM 44549 / JCM 11189.  
 RC MEDLINE=22723752; PubMed=12840036; DOI=10.1101/5r.1285603;  
 RX Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,  
 RA Sugimoto S., Matsumi K., Yamagishi A., Kikuchi H., Ikeo K.,  
 RA Gojobori T.;  
 RT "Comparative complete genome sequence analysis of the amino acid  
 RT replacements responsible for the thermostability of *Corynebacterium*  
 RL *efficiens*."; Genome Res. 13:1572-1579(2003).  
 CC -1- FUNCTION: Involved in the efflux of excess of L-lysine. This is  
 CC necessary to control the intracellular L-lysine level (By  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass  
 CC membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to the *lysE*/*argo* transporter (TC 2.A.75)  
 CC family.  
 CC -----  
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 CC -----  
 CC EMBL: AB083133; BAB88827.1; ALT INIT; Genomic DNA.  
 CC EMBL: BA000035; BAC18167.1; ALT INIT; Genomic DNA.  
 CC Genomereviews; BA000035.GR; CE1357.  
 CC DR BioCyc: CEFF196164:CE1357-MONOMER; -.  
 CC DR InterPro: IPR001123; *lysE*.  
 CC DR Pfam: PF01810; *lysE*; 1.  
 CC Complete proteome; Inner membrane; Membrane; Transmembrane; Transport.  
 CC CHAIN 1 228  
 CC FT TRANSMEM 3 23 Potential.  
 CC FT TRANSMEM 37 57 Potential.  
 CC FT TRANSMEM 66 86 Potential.  
 CC FT TRANSMEM 139 159 Potential.  
 CC FT TRANSMEM 172 192 Potential.  
 CC FT TRANSMEM 208 228 Potential.  
 CC SQ SEQUENCE 228 AA; 24374 MW; 68FB379A8380EDA7 CRC64;  
 Query Match 62.8%; Score 389.5; DB 1; Length 228;  
 Best Local Similarity 65.8%; Pred. No. 6,8e-29;  
 Matches 79; Conservative 15; Mismatches 21; Indels 5; Gaps 2;  
 QY 4 MEIFITGLLGASLLISIGPQNVLVIKQIKREGILAVLVCLISDVFIFAGTGVLL 63  
 DB 1 MEIFVTGLLGASLLISIGPQNVLVIKQIKREGITAVLVCLISDVFIFAGTGVLL 60  
 QY 64 SNAPIYVDIMRWGIAVLVFAVMAAKDAMTNKVEAPQIIETEPVDDTPGLGVF 123  
 DB 61 SDTAPITLDIRWCGIAVLVFAVMAAKDAMTNKVEAPQIIETEPVDDTPGLGVF 115  
 RESULT 5  
 LYSF\_CORDI STANDARD; PRT; 228 AA.  
 ID LYSF\_CORDI STANDARD; PRT; 228 AA.  
 AC Q6NHPI;  
 DT 11-OCT-2004, integrated into UniProtKB/Swiss-Prot.  
 DT 05-JUN-2004, sequence version 1.  
 DT 07-MAR-2006, entry version 10.  
 DE Lysine exporter protein.  
 GN Name=*lysE*; Ordered locus names=DIP1091;  
 OS *Corynebacterium diptheriae*.  
 CC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;  
 CC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.  
 CC NCBI\_TaxID=117;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).  
 RC STRAIN=Biocyte gravis / NCTC 13129;  
 RX MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gk9874;  
 RA Cerdano-Tarrega A.-M., Eferatiou A., Dover L.G., Holden M.T.G.,  
 RA Pallen M.J., Bentley S.D., Beara G.S., Churcher C.M., James K.D.,  
 RA De Zorja A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,  
 RA Hamlin N., Holtroyd S., Jagers K., Moule S., Quail M.A.,

RA Rabinowitz E., Rutherford K.M., Thomson N.R., Unwin L.,  
 RA Whitehead S., Barrett B.G., Parkhill J.;  
 RT "The complete genome sequence and analysis of *Corynebacterium*  
 RT *diptheriae* NCTC13129.";  
 CC Nucleic Acids Res. 31:6516-6523(2003).  
 CC -1- FUNCTION: Involved in the efflux of excess of L-lysine. This is  
 CC necessary to control the intracellular L-lysine level (By  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass  
 CC membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to the *lysE*/*argo* transporter (TC 2.A.75)  
 CC family.  
 CC -----  
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 CC -----  
 CC EMBL: BX248357; CAE49614.1; -; Genomic DNA.  
 CC Genomereviews; BX248353.GR; DIP1091.  
 CC DR BioCyc: CDIP117:DIP1091-MONOMER; -.  
 CC DR InterPro: IPR001123; *lysE*.  
 CC DR Pfam: PF01810; *lysE*; 1.  
 CC Complete proteome; Inner membrane; Membrane; Transmembrane; Transport.  
 CC CHAIN 1 228  
 CC FT TRANSMEM 4 26 Potential.  
 CC FT TRANSMEM 38 60 Potential.  
 CC FT TRANSMEM 65 87 Potential.  
 CC FT TRANSMEM 139 161 Potential.  
 CC FT TRANSMEM 171 193 Potential.  
 CC FT TRANSMEM 205 227 Potential.  
 CC SQ SEQUENCE 228 AA; 24662 MW; 6CSAAD0D7CB3ADE7 CRC64;  
 Query Match 43.7%; Score 271; DB 1; Length 228;  
 Best Local Similarity 47.1%; Pred. No. 1,4e-17;  
 Matches 56; Conservative 22; Mismatches 37; Indels 4; Gaps 2;  
 QY 4 MEIFITGLLGASLLISIGPQNVLVIKQIKREGILAVLVCLISDVFIFAGTGVLL 63  
 DB 1 MSINAGTGLMGLSLVAVIGPQNVLVIKQIKREGILAVLVCLISDVFIFAGTGVLL 60  
 QY 64 SNAPIYVDIMRWGIAVLVFAVMAAKDAMTNKVEAPQIIETEPVDDTPGLGV 119  
 DB 61 VDRAPIALVLMKGVAVLVLYFGTCEKAEKRGQA-LAVEGSEPVAYEVDADSSGV 118  
 RESULT 6  
 ARGO\_ECOL6 STANDARD; PRT; 211 AA.  
 ID ARGO\_ECOL6 STANDARD; PRT; 211 AA.  
 AC Q8FE55;  
 DT 11-OCT-2004, integrated into UniProtKB/Swiss-Prot.  
 DT 01-MAR-2003, sequence version 1.  
 DT 07-MAR-2006, entry version 17.  
 DE Arginine exporter protein *argo*.  
 GN Name=*argo*; Ordered locus names=c3501;  
 OS *Escherichia coli* O6.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Escherichia.  
 CC NCBI\_TaxID=217952;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).  
 RC STRAIN=OE:HI / CF703 / ATCC 700928 / UPEC.  
 RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;  
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Rosch P.,  
 RA Raeko D., Buckles E.L., Liou S.-R., Boutin A., Hackert J., Stroud D.,  
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;  
 RT "Extensive mosaic structure revealed by the complete genome sequence  
 RT of uropathogenic *Escherichia coli* O6.";  
 CC Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).  
 CC -1- FUNCTION: Involved in the export of arginine. Important to control  
 CC the intracellular level of arginine and the correct balance  
 CC between arginine and lysine (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass

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CC      membrane protein (By similarity).
CC      -|- INDUCTION: Transcriptionally regulated by argP. Lysine has a
CC      negative effect on the expression of argO (By similarity).
CC      -|- SIMILARITY: Belongs to the LysE/Argo transporter (TC 2.A.75)
CC      family.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivative license
CC      -----
DR      EMBL: AE016766; AAN81949.1; -; Genomic DNA.
DR      BioCyc: ECOLI9310:C3501-MONOMER; -
DR      HAMAP: MF_01901; -; 1.
DR      InterPro: IPR004777; Lys_exporter.
DR      InterPro: IPR001123; LysE.
DR      Pfam: PF01810; LysE; 1.
DR      TIGRfam: TIGR00948; 2a75; 1.
KM      Amino-acid transporter; Complete proteome; Inner membrane; Membrane;
KM      Transmembrane; Transport.
FT      CHAIN          1          211
FT      TRANSMEM      1          21
FT      TOPO_DOM      22         36      Cytoplasmic (Potential).
FT      TRANSMEM      37         57      Potential.
FT      TOPO_DOM      58         67      Periplasmic (Potential).
FT      TRANSMEM      68         88      Potential.
FT      TOPO_DOM      89         110     Cytoplasmic (Potential).
FT      TRANSMEM     111         131     Potential.
FT      TOPO_DOM     132         146     Periplasmic (Potential).
FT      TRANSMEM     147         167     Potential.
FT      TOPO_DOM     168         181     Cytoplasmic (Potential).
FT      TRANSMEM     182         202     Potential.
FT      TOPO_DOM     203         211     Periplasmic (Potential).
SQ      SEQUENCE      211 AA; 23174 MW; 5F22D06A3A8FBD73 CRC64;

Query Match          34.5%; Score 214; DB 1; Length 211;
Best Local Similarity 35.8%; Pred. No. 3,7e-12;
Matches 48; Conservative 27; Mismatches 41; Indels 18; Gaps 3;

QY      7 FTGGLLGASLLSTIGPQNVLVTKGIRKRGILAVLVLCISDVFLFIAGTLGVDLISNA 66
DB      5 YFGGLALGAMMILPLGPQNAFVNMQGIKROYHIMILCALISDLVLCAGIFGGSALLMQ 64
QY      67 APIVLDIMRWGIAVILMFPAVMAKDMTKVE--APQIIIE-----TEPT 110
DB      65 SPVLLALVTWVGVAFLMWGFGAFKTMSSNIELASAEVLKQGRWKIATMLAVTMLNPH 124
QY      111 VPDDT--PLGVFPG 122
DB      125 VYLDTFVVLGSLGG 138

RESULT 7
ID      Q32BY3 SHIDS PRELIMINARY; PRT; 211 AA.
AC      Q32BY3.
DT      06-DEC-2005. Integrated into UniProtKB/TrEMBL.
DT      07-FEB-2006. sequence version 1.
DE      Hypothetical protein Y9GA.
GN      Name=Y9GA; OrderedLocNames=SDY_3159;
OS      Shigella dysenteriae serotype 1 (strain Sd197).
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Shigella.
OX      NCBI_TaxID=300267;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX      PubMed=16275786; DOI=10.1093/nar/gk1954;
RA      Wang F., Yang Z., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
RA      Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
RA      Qiang B., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
RA      Qiang B., Hou Y., Yu Y., Jin Q.
RT      Genome dynamics and diversity of Shigella species, the etiologic
RT

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RT      agents of bacillary dysentery."
RL      Nucleic Acids Res. 33:6445-6458(2005).
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivative license
CC      -----
DR      EMBL: CP000034; ABB63172.1; -; Genomic DNA.
DR      GO: GO:0016021; C: integral to membrane; IEA.
DR      GO: GO:0016020; C: membrane; IEA.
DR      GO: GO:0005293; F: lysine permease activity; IEA.
DR      GO: GO:0006865; P: amino acid transport; IEA.
KM      Complete proteome; Hypothetical protein.
SQ      SEQUENCE      211 AA; 23174 MW; 5F22D06A3A8FBD73 CRC64;

Query Match          34.5%; Score 214; DB 2; Length 211;
Best Local Similarity 35.8%; Pred. No. 3,7e-12;
Matches 48; Conservative 27; Mismatches 41; Indels 18; Gaps 3;

QY      7 FTGGLLGASLLSTIGPQNVLVTKGIRKRGILAVLVLCISDVFLFIAGTLGVDLISNA 66
DB      5 YFGGLALGAMMILPLGPQNAFVNMQGIKROYHIMILCALISDLVLCAGIFGGSALLMQ 64
QY      67 APIVLDIMRWGIAVILMFPAVMAKDMTKVE--APQIIIE-----TEPT 110
DB      65 SPVLLALVTWVGVAFLMWGFGAFKTMSSNIELASAEVLKQGRWKIATMLAVTMLNPH 124
QY      111 VPDDT--PLGVFPG 122
DB      125 VYLDTFVVLGSLGG 138

RESULT 8
ID      ARGO_ECOLI STANDARD; PRT; 211 AA.
AC      P11667.
DT      01-OCT-1989. Integrated into UniProtKB/Swiss-Prot.
DT      01-OCT-1996. sequence version 2.
DT      07-MAR-2006. entry version 55.
DE      Arginine exporter protein argO.
GN      Name=argo; OrderedLocNames=b2923;
OS      Escherichia coli.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Escherichia.
OX      NCBI_TaxID=562;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX      STRAIN=K12 / MG1655;
RX      MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA      Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA      Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA      Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA      Mau B., Shao Y.
RT      "The complete genome sequence of Escherichia coli K-12."
RL      Science 277:1453-1474(1997).
RN      [2]
RP      NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 15-211.
RX      STRAIN=K12 / GS520;
RX      MEDLINE=89313302; PubMed=2546007;
RA      Alefounis P.R., Pernam R.N.
RT      Identification, molecular cloning and sequence analysis of a gene
RT      cluster encoding the class II fructose 1,6-bisphosphate aldolase, 3-
RT      phosphoglycerate kinase and a putative second glyceraldehyde 3-
RT      phosphate dehydrogenase of Escherichia coli."
RL      Mol. Microbiol. 3:723-732(1989).
RN      [3]
RP      FUNCTION.
RC      STRAIN=K12;
RX      PubMed=15150242; DOI=10.1126/JB.186.11.3539-3546.2004;
RA      Nandineni M.R., Govrishankar J.
RT      Evidence for an arginine exporter encoded by y9GA (argo) that is
RT      regulated by the LysR-type transcriptional regulator Argp in
RT      Escherichia coli."
RL      J. Bacteriol. 186:3539-3546(2004).

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RN [4]
RP TOPOLOGY.
RC STRAIN=K12 / MG1655;
RX PubMed=15919966; DOI=10.1126/science.1109730;
RA Daley D.O., Rapp M., Graneth E., Meien K., Drew D., von Heijne G.;
RT "Global topology analysis of the Escherichia coli inner membrane
RT proteome."
RT Science 308:1321-1323(2005).
CC -1- FUNCTION: Involved in the export of arginine. Important to control
CC the intracellular level of arginine and the correct balance
CC between arginine and lysine. May also be involved in the export of
CC canavanine (a plant-derived antimetabolite).
CC -1- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass
CC membrane protein.
CC -1- INDUCTION: Transcriptionally regulated by argP in response to the
CC accumulation of intracellular arginine or canavanine. Lysine has a
CC negative effect on the expression of argO.
CC -1- SIMILARITY: Belongs to the lysE/argO transporter (TC 2.A.75)
CC family.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
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CC EMBL, U28377; AAA69090.1; -; Genomic DNA.
CC EMBL, U00096; AAC75960.1; -; Genomic DNA.
CC EMBL, X14436; CAA32607.1; -; Genomic DNA.
CC PIR, B65077; OOECSA.
CC GenomeReviews: U00096_GR; b2923.
CC DR Echobase; EB1148; -.
CC DR Ecogene; EG1159; argO.
CC DR Biocyc; Ecocyc:YGA-MONOMER; -.
CC DR LinkHub; P11667; -.
CC DR HAMAP; MF_01901; -; 1.
CC DR InterPro; IPR004777; Lys exporter.
CC DR InterPro; IPR001123; LysE.
CC DR Pfam; PF01810; LysE; 1.
CC DR TIGFAMS; TIGR00948; 2a75; 1.
CC DR Amino-acid transport; Complete proteome; Inner membrane; Membrane;
CC Transmembrane; Transport.
CC KW CHAIN
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CC FT TOPO_DOM 22 36
CC FT TRANSMEM 37 57
CC FT TOPO_DOM 58 67
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CC Query Match 34.4%; Score 213; DB 1; Length 211;
CC Best Local Similarity 43.0%; Pred. No. 4.6e-12;
CC Matches 40; Conservative 21; Mismatches 32; Indels 0; Gaps 0;

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DT 21-FEB-2006, sequence version 1.
DT 07-MAR-2006, entry version 2.
DE Arginine transporter.
DE Name=argO;
OS Escherichia coli W3110.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=316407;
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=81053692; PubMed=6159575;
RA Smith D.R., Calvo J.M.;
RT "Nucleotide sequence of the E coli gene coding for dihydrofolate
RT reductase."
RL Nucleic Acids Res. 8:2255-2274(1980).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RA Sekiguchi T., Ortega-Cesena J., Nosh Y., Ohashi S., Tsuda K.,
RA Kanaya S.,
RT "DNA and amino-acid sequences of 3-isopropylmalate dehydrogenase of
RT Bacillus coagulans. Comparison with the enzymes of Saccharomyces
RT cerevisiae and Thermus thermophilus."
RL Biochim. Biophys. Acta 867:36-44(1986).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RA Chen H., Sun Y., Stark T., Beattie W., Moses R.E.;
RT "Nucleotide sequence and deletion analysis of the polB gene of
RT Escherichia coli."
RL DNA Cell Biol. 9:613-635(1990).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RA Smallshaw J.E., Kelln R.A.;
RT "Cloning, nucleotide sequence and expression of the Escherichia coli
RT K-12 pyrH gene encoding UMP kinase."
RL Genetics (Life Sci. Adv.) 11:59-65(1992).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RA Hayashi K., Murooka N., Yamamoto Y., Fujita K., Isono K., Choi S.,
RA Ohtsubo E., Baba T., Manner B.L., Mori H., Horiuchi T.;
RT "Highly accurate genome sequences of Escherichia coli K-12 strains
RT MG1655 and W3110."
RL Mol. Syst. Biol. 0:0-0(2006).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX PubMed=16397293; DOI=10.1093/nar/gk150;
RA Riley M., Abe T., Arnaud M.B., Beryl M.K., Blatter F.R.,
RA Chaudhuri R.R., Glaesner J.D., Horiuchi T., Kessler I.M., Kogure T.,
RA Mori H., Perna N.T., Plunkett G. III, Rudd K.E., Serres M.H.,
RA Thomas G.H., Thomson N.R., Wishart D., Wanner B.L.;
RT "Escherichia coli K-12: a cooperatively developed annotation snapshot-
RT 2005."
RL Nucleic Acids Res. 34:1-9(2006).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=97349980; PubMed=9205837; DOI=10.1093/dnares/4.2.91;
RA Yamamoto Y., Alda H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
RA Oshima T., Oyama S., Saito N., Sempel G., Satoh Y., Sivasubram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT K-12 genome corresponding to 50.0-68.8 min on the linkage map and
RT DNA Res. 4:91-113(1997).
RN [8]

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RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=97255359; PubMed=9097040; DOI=10.1093/dnares/3.6.379;  
 RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,  
 RA Kasai H., Kimura S., Kikawa M., Kitagawa M., Makino K., Miki T.,  
 RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,  
 RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,  
 RA Sivasubramanian S., Tagami H., Takada J., Takemoto K., Wada C.,  
 RA Yamamoto Y., Horiiuchi T.,  
 RT "A 460-bp DNA sequence of the *Escherichia coli* K-12 genome  
 RT corresponding to the 40.1-50.0 min region on the linkage map."  
 RL DNA Res. 3:379-392(1996).  
 [9]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=97255357; PubMed=9097039; DOI=10.1093/dnares/3.6.363;  
 RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,  
 RA Kasai H., Kashtamoto K., Kimura S., Kikawa M., Kitagawa M.,  
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,  
 RA Sempel G., Seki Y., Sivasubramanian S., Tagami H., Takada J.,  
 RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiiuchi T.,  
 RT "A 570-bp DNA sequence of the *Escherichia coli* K-12 genome  
 RT corresponding to the 28.0-40.1 min region on the linkage map."  
 RL DNA Res. 3:363-377(1996).  
 [10]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=97094878; PubMed=8940112; DOI=10.1074/jbc.271.49.31145;  
 RA Arn E.A., Abelson J.N.,  
 RT "The 2'-5' RNA ligase of *Escherichia coli*. Purification, cloning, and  
 RT genomic disruption."  
 RL J. Biol. Chem. 271:31145-31153(1996).  
 [11]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=97061202; PubMed=8905232; DOI=10.1093/dnares/3.3.137;  
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashtamoto K.,  
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,  
 RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
 RA Yano M., Horiiuchi T.,  
 RT "A 718-bp DNA sequence of the *Escherichia coli* K-12 genome  
 RT corresponding to the 12.7-28.0 min region on the linkage map."  
 RL DNA Res. 3:137-155(1996).  
 [12]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=94261430; PubMed=8202364;  
 RA Fujita N., Mori H., Yura T., Ishihama A.,  
 RT "Systematic sequencing of the *Escherichia coli* genome: analysis of the  
 RT 2.4-4.1 min (110,917-193,643 bp) region."  
 RL Nucleic Acids Res. 22:1637-1639(1994).  
 [13]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=94240115; PubMed=8183897;  
 RA Janosi L., Shimizu T., Kaji A.,  
 RT "Ribosome recycling factor (ribosome releasing factor) is essential  
 RT for bacterial growth."  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:4249-4253(1994).  
 [14]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=94124004; PubMed=7904973; DOI=10.1016/0378-1119(93)90470-N;  
 RA Allkmeers R., Gerrard B.C., Court D., Dean M.C.,  
 RT "Cloning and organization of the abc and mdl genes of *Escherichia*  
 RT coli: relationship to eukaryotic multidrug resistance."  
 RL Gene 136:231-236(1993).  
 [15]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;

RX MEDLINE=94018640; PubMed=8412694;  
 RA van Heeswijk W.C., Rabenberg M., Westerhoff H.V., Kahn D.D.;  
 RT "The genes of the glutamine synthetase adenylylation cascade are not  
 RT regulated by nitrogen in *Escherichia coli*."  
 RL Mol. Microbiol. 9:443-458(1993).  
 [16]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=93259920; PubMed=8387990;  
 RA Zhao S., Sandt C.H., Feulner G., Viazny D.A., Gray J.A., Hill C.W.,  
 RT "The elements of *Escherichia coli* K-12: complex composites of shared  
 RT and unique components that have different evolutionary histories."  
 RL J. Bacteriol. 175:2799-2808(1993).  
 [17]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=93123180; PubMed=8419307;  
 RA Yamada M., Asaoka S., Sater M.H., Jr., Yamada Y.,  
 RT "Characterization of the *gcd* gene from *Escherichia coli* K-12 W3110 and  
 RT regulation of its expression."  
 RL J. Bacteriol. 175:568-571(1993).  
 [18]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=93116053; PubMed=1474579;  
 RA Cormack R.S., Mackie G.A.,  
 RT "Structural requirements for the processing of *Escherichia coli* 5 S  
 RT ribosomal RNA by RNase E in vitro."  
 RL J. Mol. Biol. 228:1078-1090(1992).  
 [19]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=93094132; PubMed=1459551;  
 RA Gervais F.G., Drapeau G.R.,  
 RT "Identification, cloning, and characterization of *rcsf*, a new  
 RT regulator gene for exopolysaccharide synthesis that suppresses the  
 RT division mutation *ftsZ84* in *Escherichia coli* K-12."  
 RL J. Bacteriol. 174:8016-8022(1992).  
 [20]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=93077430; PubMed=1447125;  
 RA Yamanaka K., Ogura T., Niki H., Hiraoka S.,  
 RT "Identification and characterization of the *smh* gene, a suppressor of  
 RT the *mukB* null mutant of *Escherichia coli*."  
 RL J. Bacteriol. 174:7517-7526(1992).  
 [21]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-12;  
 RX MEDLINE=93011013; PubMed=1396599;  
 RA Condon C., Phillips J., Fu Z.Y., Squires C., Squires C.L.,  
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 RT Matches 40; Conservative 21; Mismatches 32; Indels 0; Gaps 0;  
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 Db 5 YFGALGALGAMTLPFGPQVAFVNGIRYRHYIMTALCAISDLVLCIGRFGSALLMO 64  
 QY 67 APIVDIMRGGIAVLVFAVMAKADMTNKE 99  
 Db 65 SPWLALVYMGVAFVFLWYGFQAFRTASSNIE 97  
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 AC Q3YXU9;  
 DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.  
 DT 27-SEP-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 5.  
 DE Hypothetical protein y99A.

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GN Name=yggA; Ordered locusNames=SSO_3075; ORFNames=SSO_3075;
OS Shigella sonnei (strain S6046).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
NCBI_TaxID=300269;
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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16275786; DOI=10.1093/nar/gki1954;
RA Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
RA Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
RA Nie H., Peng Y., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
RA Qiang B., Hou Y., Yu J., Jin Q.;
RT "Genome dynamics and diversity of Shigella species, the etiologic
RT agents of bacillary dysentery."
RL Nucleic Acids Res. 33:6445-6458(2005).
CC
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CC -----
DR EMBL, CP000038; AA289663.1; -; Genomic DNA.
DR GO, GO:0016021; C:integral to membrane; IEA.
DR GO, GO:0016020; C:membrane; IEA.
DR GO, GO:0005293; F:lysine permease activity; IEA.
DR GO, GO:0006865; P:amino acid transport; IEA.
DR InterPro, IPR003016; Lipoyl BS.
DR InterPro, IPR004777; Lys exporter.
DR InterPro, IPR001123; LysE.
DR Pfam, PF01810; LysE; 1.
DR TIGRFAMs, TIGR00948; 2a75; 1.
DR PROSITE, PS00189; LIPOYL; UNKNOWN.1.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 211 AA; 23174 MW; DC946439D9EB920 CRC64;

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RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796; DOI=10.1093/dnares/8.1.11;
RA Hayashi T., Makino K., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohnubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Saekawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
CC
CC -1- FUNCTION: Involved in the export of arginine. Important to control
CC the intracellular level of arginine and the correct balance
CC between arginine and lysine (by similarity).
CC -1- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass
CC membrane protein (By similarity).
CC -1- INDUCTION: Transcriptionally regulated by argP. Lysine has a
CC negative effect on the expression of argO (By similarity).
CC -1- SIMILARITY: Belongs to the LysE/argO transporter (TC 2.A.75)
CC family.
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DR EMBL, AE005174; AAG58049.1; -; Genomic DNA.
DR EMBL, BA000007; BAB37217.1; -; Genomic DNA.
DR PIR, B91103; B91103.
DR PIR, B85948; B85948.
DR GenomeReviews, BA000007 GR; EC63794.
DR GenomeReviews, AE005174 GR; 24260.
DR BioCyc, ECOL3334-1:EC63794-MONOMER; -.
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DR InterPro, IPR004777; Lys_exporter.
DR InterPro, IPR001123; LysE.
DR Pfam, PF01810; LysE; 1.
DR TIGRFAMs, TIGR00948; 2a75; 1.
DR Complete proteome; Inner membrane; Membrane;
DR Amino-acid transporter; Complete proteome; Inner membrane; Membrane;
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FT TRANSMEM 37..57 Potential.
FT TOPO_DOM 58..67 Periplasmic (Potential).
FT TRANSMEM 68..88 Potential.
FT TOPO_DOM 89..110 Cytoplasmic (Potential).
FT TRANSMEM 111..131 Potential.
FT TOPO_DOM 132..146 Periplasmic (Potential).
FT TRANSMEM 147..167 Potential.
FT TOPO_DOM 168..181 Cytoplasmic (Potential).
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FT TOPO_DOM 203..211 Periplasmic (Potential).
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DT 11-OCT-2004, integrated into UniProtKB/Swiss-Prot.  
DT 01-MAR-2002, sequence version 1.  
DE Arginine exporter protein argo.  
GN Name=argo; OrderedLocustNames=STY3222, t2984;  
OS Salmonella typhi.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Salmonella.  
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RN (1)  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=CT18;  
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1093/35101607;  
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,  
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jogle K.,  
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Goza P., Parry C.,  
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,  
RA Whitehead S., Barrett B.G.;  
RA "Complete genome sequence of a multiple drug resistant Salmonella  
RT enterica serovar Typhi CT18.";  
RL Nature 413:848-852(2001).  
RN (2)  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=Ty2 / ATCC 700931;  
RX MEDLINE=22531367; PubMed=12644504;  
RX DOI=10.1128/JB.185.7.2330-2337.2003;  
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,  
RA Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;  
RA "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2  
RT and CT18.";  
RL J. Bacteriol. 185:2330-2337(2003).  
CC -!- FUNCTION: Involved in the export of arginine. Important to control  
CC the intracellular level of arginine and the correct balance  
CC between arginine and lysine (By similarity).  
CC -!- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass  
CC membrane protein (By similarity).  
CC -!- SIMILARITY: Belongs to the LysE/argo transporter (TC 2.A.75)  
CC family.  
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CC Distributed under the Creative Commons Attribution-NonDerivs license  
CC -----  
CC EMBL, AL627277; CAD02896.1; -; Genomic DNA.  
CC EMBL, AE014613; AA070536.1; -; Genomic DNA.  
CC GenomeReviews; AL513382.GR; STY3222.  
CC GenomeReviews; AE014613.GR; t2984.  
CC BioCyc; SENT09261:TY984-MONOMER; -;  
CC BioCyc; SENT90370:STY3222-MONOMER; -;  
CC HAMAP; MF\_01901; -; 1.  
CC InterPro; IPR004777; LysE exporter.  
CC InterPro; IPR001123; LysE.  
CC Pfam; PF01810; LysE; 1.  
CC TIGRFAMs; TIGR00948; 2a75; 1.  
KW Amino-acid transporter; Complete proteome; Inner membrane; Membrane;  
KW Transmembrane; Transp.

FT TOPO DOM 200 211 Periplasmic (Potential).  
SQ SEQUENCE 211 AA; 23172 MW; 13CB427CABE5A3FC CRC64;  
Query Match 33.1%; Score 205; DB 1; Length 211;  
Best Local Similarity 38.1%; Pred. No. 2,6e-11;  
Matches 37; Conservative 26; Mismatches 34; Indels 0; Gaps 0;  
Qy 3 IMEFTGLGASLLSIPQVLYIKQIGREGIAYLVLCISDPFPIGTGVDL 62  
Db 1 MISTYFGVALGAMLPQGPQAFVMOGIRQYHMLALCALDVLISAGIFGSA 60  
Qy 63 LSNAPIVDINMGSIAYLVLPFAVMAAKDAMTKYE 99  
Db 61 LMQSPMLALVTVGSAFLVWFGALTKTANSNIE 97  
RESULT 15  
ID ARGO\_SALCH STANDARD; PRT; 211 AA.  
AC 057K48;  
DT 25-OCT-2005, integrated into UniProtKB/Swiss-Prot.  
DT 10-MAY-2005, sequence version 1.  
DT 07-MAR-2006, entry version 8.  
DE Arginine exporter protein argo.  
GN Name=argo; OrderedLocustNames=SC3008;  
OS Salmonella choleraesuis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Salmonella.  
OX NCBI\_TaxId=591;  
RN (1)  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=SC-867;  
RX PubMed=15781495; DOI=10.1093/nar/gk1297;  
RX Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,  
RA Wang H.-S., Lee Y.-S.;  
RA "The genome sequence of Salmonella enterica serovar Choleraesuis, a  
RT highly invasive and resistant zoonotic pathogen.";  
RL Nucleic Acids Res. 33:1690-1698(2005).  
CC -!- FUNCTION: Involved in the export of arginine. Important to control  
CC the intracellular level of arginine and the correct balance  
CC between arginine and lysine (By similarity).  
CC -!- SUBCELLULAR LOCATION: Bacterial cell inner membrane; multi-pass  
CC membrane protein (By similarity).  
CC -!- SIMILARITY: Belongs to the LysE/argo transporter (TC 2.A.75)  
CC family.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NonDerivs license  
CC -----  
CC EMBL, AE017220; AA66914.1; -; Genomic DNA.  
CC GenomeReviews; AE017220.GR; SC3008.  
CC HAMAP; MF\_01901; -; 1.  
CC InterPro; IPR004777; LysE exporter.  
CC InterPro; IPR001123; LysE.  
CC Pfam; PF01810; LysE; 1.  
CC TIGRFAMs; TIGR00948; 2a75; 1.  
KW Amino-acid transporter; Complete proteome; Inner membrane; Membrane;  
KW Transmembrane; Transp.

FT TRANSMEM 1 21 Arginine exporter protein argo.  
FT TRANSMEM 37 57 Potential.  
FT TRANSMEM 68 88 Potential.  
FT TRANSMEM 111 131 Potential.  
FT TRANSMEM 147 167 Potential.  
FT TRANSMEM 179 199 Potential.  
SQ SEQUENCE 211 AA; 23239 MW; 64D6E26F0B371D0F CRC64;  
Query Match 32.9%; Score 204; DB 1; Length 211;  
Best Local Similarity 38.1%; Pred. No. 3.3e-11;  
Matches 37; Conservative 25; Mismatches 35; Indels 0; Gaps 0;  
Qy 3 IMEFTGLGASLLSIPQVLYIKQIGREGIAYLVLCISDPFPIGTGVDL 62

Db 1 MISTYFQGFALGAMMILPLGPNAPVMMQGIROTHMLIALLCALSDLVLSAGIFGGA 60  
QY 63 LSNAPIVLDIMRWGIAVLLMFVMAKADAMTNKVE 99  
Db 61 LMQSPWLLALVTWGVAFLLWGFGLKXTAMSSNLE 97

Search completed: July 19, 2006, 00:30:30  
Job time : 302 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2006, 00:30:55 ; Search time 51 Seconds  
(without alignments)  
212.820 Million cell updates/sec

Title: US-10-716-470-10

Perfect score: 620  
Sequence: 1 MVMIEIFITGLLGLASLLLS.....ETEPPTVDDPTPLGVFGGQH 124

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/5.COMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/6.COMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/7.COMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/H.COMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/PGTUS.COMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/RE.COMB.pep:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	584	94.2	236	US-09-105-117K-2	Sequence 2, Appli
2	215	34.7	211	US-09-459-573-16	Sequence 16, Appli
3	205	33.1	213	US-09-489-039A-11845	Sequence 11845, A
4	185	29.8	214	US-09-543-681A-4972	Sequence 4972, Ap
5	172.5	27.8	232	US-09-252-991A-24479	Sequence 24479, A
6	158	25.5	211	US-09-328-352-5737	Sequence 5737, Ap
7	112	18.1	211	US-09-902-540-9913	Sequence 9913, Ap
8	109	17.6	219	US-09-489-039A-7731	Sequence 7731, Ap
9	99.5	16.0	212	US-09-543-681A-767	Sequence 767, Ap
10	93.5	15.1	235	US-09-328-352-8249	Sequence 8249, Ap
11	90.5	14.6	208	US-09-328-352-5111	Sequence 5111, Ap
12	88.5	14.3	212	US-09-459-573-12	Sequence 12, Appli
13	88	14.2	211	US-09-489-039A-9608	Sequence 9608, Ap
14	86.5	14.0	205	US-09-489-039A-12661	Sequence 12661, A
15	86	13.9	206	US-09-252-991A-18746	Sequence 18746, A
16	86	13.9	260	US-09-252-991A-25992	Sequence 25992, A
17	83.5	13.5	210	US-09-328-352-4775	Sequence 4775, Ap
18	83.5	13.5	222	US-09-252-991A-26644	Sequence 26644, A
19	83	13.4	552	US-09-489-039A-7419	Sequence 7419, Ap
20	80.5	13.0	228	US-09-543-681A-4854	Sequence 4854, Ap
21	79.5	12.8	205	US-09-396-357-2	Sequence 2, Appli
22	79.5	12.8	205	US-09-847-392-2	Sequence 2, Appli
23	79.5	12.8	221	US-09-328-352-6659	Sequence 6659, Ap
24	79.5	12.8	250	US-09-543-681A-4487	Sequence 4487, Ap
25	79	12.7	212	US-09-248-796A-20354	Sequence 20354, A
26	77.5	12.5	195	US-09-459-573-14	Sequence 14, Appli

27	77.5	12.5	249	US-09-252-991A-25717	Sequence 25717, A
28	76.5	12.3	217	US-09-489-039A-8076	Sequence 8076, Ap
29	75	12.1	316	US-09-540-236-3467	Sequence 3467, Ap
30	74.5	12.0	1172	US-09-328-352-6071	Sequence 6071, Ap
31	74	11.9	203	US-09-252-991A-16947	Sequence 16947, A
32	74	11.9	312	US-09-252-991A-22091	Sequence 22091, A
33	73.5	11.9	214	US-09-489-039A-9793	Sequence 9793, Ap
34	73.5	11.9	238	US-09-328-352-7122	Sequence 7122, Ap
35	73.5	11.8	464	US-09-489-039A-9621	Sequence 9621, Ap
36	73	11.8	222	US-09-328-352-6471	Sequence 6471, Ap
37	73	11.8	237	US-09-252-991A-27175	Sequence 27175, A
38	72.5	11.7	256	US-09-270-767-47525	Sequence 47525, A
39	72	11.6	211	US-09-252-991A-20747	Sequence 20747, A
40	72	11.6	427	US-09-721-870-115	Sequence 115, App
41	72	11.6	434	US-09-721-870-117	Sequence 117, App
42	72	11.6	446	US-09-602-787A-426	Sequence 426, App
43	71.5	11.5	223	US-09-459-573-10	Sequence 10, Appli
44	71.5	11.5	461	US-09-248-796A-23597	Sequence 23597, A
45	70.5	11.4	257	US-09-560-761B-12	Sequence 12, Appli

## ALIGNMENTS

```

RESULT 1
US-09-105-117K-2
; Sequence 2, Application US/09105117K
; Patent No. 6858406
; GENERAL INFORMATION:
; APPLICANT: Forschungszentrum Juelich GmbH; Marina Vrljic et al.
; TITLE OF INVENTION: Process for the microbial production of amino acids by
; TITLE OF INVENTION: Boosted activity of export carriers
; FILE REFERENCE: 1
; CURRENT APPLICATION NUMBER: US/09/105,117K
; CURRENT FILING DATE: 1996-06-17
; PRIOR APPLICATION NUMBER: PCT/DE96/02485
; PRIOR FILING DATE: 1996-12-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; OTHER INFORMATION: (lyse)
US-09-105-117K-2

Query Match          94.2%; Score 584; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MVMIEIFITGLLGLASLLISGPQNVLYIKGIRREGIAVLVCLSDVFLTAGTGV 60
DB      1 MVMIEIFITGLLGLASLLISGPQNVLYIKGIRREGIAVLVCLSDVFLTAGTGV 60

QY      61 DLISNAPIYVDINRWGIAVLVFAVMAAKADMTNKVAPQIEETPTVDDPTPLG 118
DB      61 DLISNAPIYVDINRWGIAVLVFAVMAAKADMTNKVAPQIEETPTVDDPTPLG 118

RESULT 2
US-09-459-573-16
; Sequence 16, Application US/09459573
; Patent No. 6979560
; GENERAL INFORMATION:
; APPLICANT: LIVSHITS, VITALITY
; APPLICANT: ZAKATAEVA, NATALIA
; APPLICANT: NAKANISHI, KAZUO
; APPLICANT: VENIAMINOVICH, VLADIMIR
; APPLICANT: TROSHIN, PETR
; APPLICANT: TOKMAKOVA, IRINA
; TITLE OF INVENTION: METHOD FOR PRODUCING L-AMINO ACIDS
; FILE REFERENCE: 0010-1066-0

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; CURRENT APPLICATION NUMBER: US/09/459,573
; CURRENT FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: RU98124016
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: RU99104431
; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-459-573-16

Query Match          34.7%; Score 215; DB 2; Length 211;
Best Local Similarity 41.2%; Pred. No. 1.3e-19;
Matches 40; Conservative 22; Mismatches 35; Indels 0; Gaps 0;

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QY 3 IMEIFITGLLGASLLISIGPQNVLVIKQIKREGGLAVLVCLISDVFLFIAGTLGVDL 62
DB 1 VFSYFQGLALGAMILPLIGPQNAFVWNGIRQYHIMIALCISDLVLCAGIFGSA 60
QY 63 LSNAAPVLDIMRWGGIAYILMFVMAAKDAMTKVE 99
DB 61 LMQSPWLLALVTWGVAFLLWVGAFKXTAMSSNIE 97

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```

RESULT 3
US-09-489-039A-11845
; Sequence 11845, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11845
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11845

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Query Match          33.1%; Score 205; DB 2; Length 213;
Best Local Similarity 37.4%; Pred. No. 2.7e-18;
Matches 37; Conservative 25; Mismatches 37; Indels 0; Gaps 0;

QY 1 MVIMEIFITGLLGASLLISIGPQNVLVIKQIKREGGLAVLVCLISDVFLFIAGTLGV 60
DB 1 ILMFTYFQGLALGAMILPLIGPQNAFVWNGIRQYHIMIALCISDLVLCAGIFGSA 60
QY 61 DLISNAPVLDIMRWGGIAYILMFVMAAKDAMTKVE 99
DB 61 SALMQSPWLLALVTWGVAFLLWVGAFKXTAFSGSL 99

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RESULT 4
US-09-543-681A-4972
; Sequence 4972, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09

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; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4972
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4972

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Query Match          29.8%; Score 185; DB 2; Length 214;
Best Local Similarity 36.0%; Pred. No. 1.1e-15;
Matches 36; Conservative 22; Mismatches 42; Indels 0; Gaps 0;

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QY 3 IMEIFITGLLGASLLISIGPQNVLVIKQIKREGGLAVLVCLISDVFLFIAGTLGVDL 62
DB 8 MLTTFQGLFLSAAMILPLIGPQNAFVLQSGSKQYHLMMSAFLLCALSIVILLISGVFPGSA 67
QY 63 LSNAAPVLDIMRWGGIAYILMFVMAAKDAMTKVEAPQ 102
DB 68 LLSQSEYLLILITWGVAFLLWVGAFKXTAFKTELSQL 107

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RESULT 5
US-09-252-991A-24479
; Sequence 24479, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24479
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24479

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```

Query Match          27.8%; Score 172.5; DB 2; Length 232;
Best Local Similarity 35.7%; Pred. No. 5e-14;
Matches 35; Conservative 20; Mismatches 38; Indels 5; Gaps 1;

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QY 7 FITGLLGASLLISIGPQNVLVIKQIKREGGLAVLVCLISDVFLFIAGTLGVDL 66
DB 37 YNGLIYAGGLIITIGAQNAPVLAQSLRREHLSVALCVCDAVLVSLGVFLATLLE 96
QY 67 APIVLDIMRWGGIAYILMFVMAAKDAMTKVE 99
DB 97 NPTLAIARWGGIAYILWGLKALLRALRPDALGNAAE 134

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```

RESULT 6
US-09-328-352-5737
; Sequence 5737, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5737
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5737

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Query Match 25.5%; Score 158; DB 2; Length 211;  
 Best Local Similarity 32.6%; Pred. No. 3.3e-12;  
 Matches 29; Conservative 25; Mismatches 35; Indels 0; Gaps 0;

QY 1 MWMEITITGLGASLLSIGPQNVLYKQIGREGIAVLVCLISDVFLFIAGTLGV 60  
 DB 12 MSLSVFKEKIGIGSGIIVAGIQAQNAFVLKQGLKQYVFMCLICALSDSLIACGVIGF 71

QY 61 DLSSNAPIVLDIRMGIAVLLWFAVMA 89  
 DB 72 AEIMTASPLITAKYIGATFLFYGAKA 100

RESULT 7  
 US-09-902-540-9913  
 ; Sequence 9913, Application US/09902540  
 ; Patent No. 6833447  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Goldman, Barry S.  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; APPLICANT: Wiegand, Roger C.  
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
 ; FILE REFERENCE: 38-10(15849)B  
 ; CURRENT APPLICATION NUMBER: US/09/902,540  
 ; CURRENT FILING DATE: 2001-07-10  
 ; PRIOR APPLICATION NUMBER: 60/217,883  
 ; PRIOR FILING DATE: 2000-07-10  
 ; NUMBER OF SEQ ID NOS: 16825  
 ; SEQ ID NO 9913  
 ; LENGTH: 211  
 ; TYPE: PRF  
 ; ORGANISM: Myxococcus xanthus  
 US-09-902-540-9913

Query Match 18.1%; Score 112; DB 2; Length 211;  
 Best Local Similarity 25.6%; Pred. No. 3.1e-06;  
 Matches 23; Conservative 26; Mismatches 35; Indels 6; Gaps 3;

QY 16 SLLSIGPQNVLYKQIGI---KREGIAVLVCLISDVFLFIAGTLGVLLSAAPIVD 72  
 DB 17 ALITGPPTMFVLARSKQGRKAGIVSALGT-FVGLFHIAAAGSLTSLATSALAPS 75

QY 73 IMRWGIAVLLWFAV---MAKADMTNKVEA 100  
 DB 76 VVKMGGAAYLVWVGVMKRSKDTVAEAVQA 105

RESULT 8  
 US-09-489-039A-7731  
 ; Sequence 7731, Application US/09489039A  
 ; Patent No. 6610836  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary Breton et. al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 2709.2004001  
 ; CURRENT APPLICATION NUMBER: US/09/489,039A  
 ; CURRENT FILING DATE: 2000-01-27  
 ; PRIOR APPLICATION NUMBER: US 60/117,747  
 ; PRIOR FILING DATE: 1999-01-29  
 ; NUMBER OF SEQ ID NOS: 14342  
 ; SEQ ID NO 7731  
 ; LENGTH: 219  
 ; TYPE: PRF  
 ; ORGANISM: Klebsiella pneumoniae  
 US-09-489-039A-7731

Query Match 17.6%; Score 109; DB 2; Length 219;  
 Best Local Similarity 27.9%; Pred. No. 8.1e-06;  
 Matches 29; Conservative 20; Mismatches 45; Indels 10; Gaps 3;

QY 7 FITGLLAGSLLSIGPQNVLYKQIGI---REGIAVLVCLISDVFLFIAGTLGVLL 63

DB 17 YLYLVGAVAILLPBGNPFVLKGTIAGVKKGYLLAAGV-FIGDAVLMFLAFAGVATL 75  
 QY 64 SNAPIVLDIRMGIAVLLM-----FAVMAKADMTNKVEAP 101  
 DB 76 IKTPVLFVNVRYLGAIVLLMGLGKMLYAVLITRDQSDASAP 119

RESULT 9  
 US-09-543-681A-4767  
 ; Sequence 4767, Application US/09543681A  
 ; Patent No. 6605709  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GARY BRETON  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRAB.  
 ; FILE REFERENCE: 2709.1002-001  
 ; CURRENT APPLICATION NUMBER: US/09/543,681A  
 ; CURRENT FILING DATE: 2000-04-05  
 ; PRIOR APPLICATION NUMBER: US 60/128,706  
 ; PRIOR FILING DATE: 1999-04-09  
 ; NUMBER OF SEQ ID NOS: 8344  
 ; SEQ ID NO 4767  
 ; LENGTH: 212  
 ; TYPE: PRF  
 ; ORGANISM: Proteus mirabilis  
 US-09-543-681A-4767

Query Match 16.0%; Score 99.5; DB 2; Length 212;  
 Best Local Similarity 27.6%; Pred. No. 0.00013;  
 Matches 27; Conservative 26; Mismatches 38; Indels 7; Gaps 3;

QY 5 EEIFGLLAGSLLSIGPQNVLYKQIGI---REGIAVLVCLISDVFLFIAGTLGV 61  
 DB 17 DIFLSAIFSVYTSITPGNNIMLLASGINFGLKRTMPRAIGVSGFFVLLAVG-IGIG 75

QY 62 LLSNAPIVLDIRMGIAVLLWFAVMAKADMTNKVE 99  
 DB 76 ALIKSPITVNLKLYGALYLLM---LWKTAISHSVE 110

RESULT 10  
 US-09-328-352-8249  
 ; Sequence 8249, Application US/09328352  
 ; Patent No. 6562958  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary L. Breton et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
 ; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: GTC99-03PA  
 ; CURRENT APPLICATION NUMBER: US/09/328,352  
 ; CURRENT FILING DATE: 1999-06-04  
 ; NUMBER OF SEQ ID NOS: 8252  
 ; SEQ ID NO 8249  
 ; LENGTH: 235  
 ; TYPE: PRF  
 ; ORGANISM: Acinetobacter baumannii.  
 US-09-328-352-8249

Query Match 15.1%; Score 93.5; DB 2; Length 235;  
 Best Local Similarity 27.3%; Pred. No. 0.00092;  
 Matches 33; Conservative 21; Mismatches 54; Indels 13; Gaps 5;

QY 3 IMEIFITGLGASLLSIGPQNVLYKQIGIKREGIAVLV---CLISDVFLFIAGTLG 59  
 DB 29 LSQILAFGLIC-LAMVLPBPNMYYLISRSIS--QGIAGFISLGVAVGFVYMLCASFG 86

QY 60 VDLSSNAPIVLDIRMGIAVLLWFAVMAKADMTNKVEAPQIIEETPTVPDPTLGV 119  
 DB 87 ITALVAVPVAIVDIRIAGVAYLLMLAKLRP-----NAPIFNVADLAV--DSPILK 138

QY 120 F 120

[illegible][illegible]

RESULT 15  
US-09-1252-991A-18746  
; Sequence 18746, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc Y. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252.991A  
 ; PRIORITY FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 18746  
 ; LENGTH: 206  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 ; US-09-252-991A-18746

Query Match 13.9%; Score 86; DB 2; Length 206;  
 Best Local Similarity 27.0%; Pred. No. 0.0072;  
 Matches 34; Conservative 17; Mismatches 51; Indels 24; Gaps 6;

QY	4	MEIFITGLLGASLLISIGPONVLTQKIGKREGLIA---VLTVCILISDVFLFIAGTIG	59
DB	10	MOSLVFPLFAVVASITPPTNLTLSNS-QRHGLAAMPYIVGACAAVAALILLG-LG	67
QY	60	VDLSNADPIVDIMRW---GGIAYLLMFAVMAAKDAMTNKVEAPQIIETEPTVPDDTP	116
DB	68	IGELLRRHPLLOGLAMLVGWLSTYLAWSLFRSAGS-----IDGAEP---PRR	112
QY	117	LGVPFG 122	
DB	113	LGVLGG 118	

Search completed: July 19, 2006, 00:32:11  
 Job time : 52 secs

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November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).



```

: CURRENT FILING DATE: 2005-02-14
: PRIOR APPLICATION NUMBER: 60/544,190
: PRIOR FILING DATE: 2004-02-13
: NUMBER OF SEQ ID NOS: 119966
: SEQ ID NO 7128
: LENGTH: 226
: TYPE: prt
: ORGANISM: Zea mays subsp. mays
: FEATURE:
: NAME/KEY: peptide
: LOCATION: (1)..(226)
: OTHER INFORMATION: Ceres Seq. ID no. 12357352
: OS-11-056-355B-7128

```

Query Match	14.7%	Score 91;	DB 7;	Length 226;
Best Local Similarity	23.8%	Pred. NO. 0.02;		
Matches 25;	Conservative 26;	Mismatches 40;	Indels 14;	Gaps 5

```
QY      3 IMEPIITGLLIGASLLSTLSPONVLTLYKQIK---REGIAYLVLCILISVPFIAGTLG 59
        ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db     105 IMPIALTGLLIIMFPLL-IATNANIVTSALMSLAAGGFIAIFACTIVA-VYI---GAVG 159
        ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY      60 VDLSSNAPIVIDIM-----RWGGIAYLILFPVMMAKAQMNTKV 98
        ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db     160 VAIPFISAIVISSVVGMITTGVGEFMIMWFAARSKMDITTKSI 204
        ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
```

```

RESULT 3
US-11-056-355B-7127
Sequence 7127, Application US/11056355B
Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brewer, Vyacheslav
APPLICANT: Alexandrov, Nikolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 7127
LENGTH: 250
TYPE: pTc
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: peptide
LOCATION: (1)..(250)
OTHER INFORMATION: Ceres Seq. ID no. 12357351
US-11-056-355B-7127

```

Query Match	14.7%	Score 91	DB 7	Length 250
Best Local Similarity	23.6%	Pred. No. 0.022		
Matches	25	Conservative	26	Mismatches 40; Indels 14; Gaps 5

  

QY	3	IMEFTIGLLGASLLSISGPONLVYKQGIK---	REGIIAVLVYCLISDPLFIAGTIG	59
DB	129	IMFALTKLLFMFELL-IATNNAIVTALSLSLAAGGELAFACLVAA-VYI---	GAVG	183
QY	60	VDLSNNAPIVLDIR---	RWGIIAYLWFAVNAARDAMTKV	98
DB	184	VAIRAIASIVISSVVGWMITTGWGFFPMWIMWTARKSDLTGSI	228	

RESULT 4  
US-11-199-489A-72  
; Sequence 72, Application US/11199489A  
; Publication No. US20060134745A1  
; GENERAL INFORMATION:  
; APPLICANT: Klenhammer, Todd R.  
; APPLICANT: Russell, William M.  
; APPLICANT: Altermann, Eric

```

: TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
: TITLE OF INVENTION: TWO-COMPONENT SENSING AND REGULATORY PROTEINS, ANTIMICROBIAL
: TITLE OF INVENTION: PROTEINS AND USES THEREFOR
: FILE REFERENCE: 035051/225793
: CURRENT APPLICATION NUMBER: US/11/199,489A
: CURRENT FILING DATE: 2005-08-08
: PRIOR APPLICATION NUMBER: 60/599,972
: PRIOR FILING DATE: 2004-08-04
: NUMBER OF SEQ ID NOS: 180
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 72
: LENGTH: 452
: TYPE: PRT
: ORGANISM: Lactobacillus acidophilus
US-11-199-489A-72

Query Match      14.4%  Score 89.5:  DB 7:  Length 452;
Best Local Similarity 22.4%:  Pred. No. 0.065;
Matches      35:  Conservative 29;  Mismatches 39;  Indels 53;  Gaps 6;

```

Query Match	14.4%	Score 89.5	DB 7	Length 452
Best Local Similarity	22.4%	Pred. No. 0.055		
Matches	35	Conservative	29	Mismatches 39; Indels 53; Gaps 6

  

QY	7	FITGLLGASLL	-----	SIGPONTVLVKQ	31
		: : : : : :		: : : : :	
Db	108	FVTLGLTALLILEENPLHLGAKATYQDAAPFRITISGAPIVSIIIPQN	-----	LIRTE	166
		: : : : : :		: : : : :	
QY	32	GIRKEGLIA	---VLLVCLISDVLEFI	---AGTLGVDLISNAPLYLDIMRWGGLAYLLWF	85
		: : : : : :	: : : : : :	: : : : : :	
Db	167	GLATQGMIAFWTGTITIAIILDPRIPLFVFKMGALIGVAINITGVLTDI	-----	ILTY	218
		: : : : : :		: : : : :	
QY	86	AYMAAKDAMTKNKEAPQIETETETVVDOTPLGVPFG			121
		: : : : : :			
Db	219	YVLCKTEYIKIKLKRYTKI	---SGRTIYDAIVAGIPG		251
		: : : : : :	: : : : : :		

```

RESULT 5
US-11-056-355B-5157
? Sequence 5157, Application US/11056355B
? Publication No. US20060150283A1
? GENERAL INFORMATION:
? APPLICANT: Brover, Vyacheslav
? APPLICANT: Alexandrov, Nikolai
? TITLE OR INVENTION: Sequence Determined DNA Fragments and Corresponding
? FILE REFERENCE: 2750-1590P052
? CURRENT APPLICATION NUMBER: US/11/056,355B
? CURRENT FILING DATE: 2005-02-14
? PRIOR APPLICATION NUMBER: 60/244,190
? PRIOR FILING DATE: 2004-02-13
? NUMBER OF SEQ ID NOS: 119966
? SEQ ID NO 5157
? LENGTH: 452
? TYPE: prt
? ORGANISM: Zea mays subsp. mays
? FEATURE:
? NAME/KEY: peptide
? LOCATION: (1)..(452)
? OTHER INFORMATION: Ceres Seq. ID no. 12409681
? US-11-056-355B-5157

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Query Match: 12.9%; Score 80; DB 7; Length 452;
Best Local Similarity 27.5%; Pred. No. 0.7;
Matches 33; Conservative 19; Mismatches 40; Indels 28; Gaps 6

QY      14 GASLLSLSTGPONVLYIKGK--REGILAVL-----LVCLISVPLP---IAGTLGVPL 62
          |||..|||..|||..|||..|||..|||..|||..|||..|||..|||..|||..|||..
Db      47 GSSDMLQVTVETILAVNACAPREFKRLAALREDVACAPAAHLLTLIDVARKGVPT 106
          |||..|||..|||..|||..|||..|||..|||..|||..|||..|||..|||..|||..
QY      63 LSNAPILVLDIMRWGILAYLLIFAVMA-----KAAMTKYEAPOIIEETETVFDPT 116
          |||..|||..|||..|||..|||..|||..|||..|||..|||..|||..|||..|||..
Db      107 L-----ALRGSAAACLMFAAFALCDKGVPQKOSQLEAP--VTELPRYVRDLP 155
          |||..|||..|||..|||..|||..|||..|||..|||..|||..|||..|||..|||..

```

RESULT 6  
US-11-056-355B-5156

```

; Sequence 5156, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; NUMBER OF SEQ ID NOS: 119966
; LENGTH: 484
; TYPE: prt
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(484)
; OTHER INFORMATION: Ceres Seq. ID no. 12409680
US-11-056-355B-5156

```

```

Query Match      12.2%; Score 80; DB 7; Length 484;
Best Local Similarity 27.5%; Pred. No. 0.76;
Matches 33; Conservative 19; Mismatches 40; Indels 28; Gaps 6;

```

```

QY 14 GASLLSTIGPQNVLVKQKIGK--REGLIIVL---LVCLISDVFLF---IAGTIGVDL 62
DB 79 GSSDALQVVERIVLVNRAACEAPFRERLALALAREDVACLVAAHALLTLIDVARGLGVP 138
QY 63 LSNAPRIVDIMEWGIAVYLLMFVAVMAA-----KQAMTKVEAPQIIEETPTVPDPPT 116
DB 139 L-----VLTGSAACLRMPAPALPCDKGYQAPQESQLERP--VTLPYPRYRDLPT 187

```

```

RESULT 7
US-11-351-137A-2
; Sequence 2, Application US/11351137A
; Publication No. US20060148041A1
; GENERAL INFORMATION:
; APPLICANT: MAIER, THOMAS
; TITLE OF INVENTION: METHOD FOR FERMENTATIVE PRODUCTION OF AMINO ACIDS AND AMINO
; FILE REFERENCE: MAIER, T-2
; CURRENT APPLICATION NUMBER: US/11/351,137A
; PRIOR FILING DATE: 2006-02-09
; PRIOR APPLICATION NUMBER: GERMAN NO. 102 32 930.3
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 195
; TYPE: prt
; ORGANISM: Escherichia coli
US-11-351-137A-2

```

```

Query Match      12.5%; Score 77.5; DB 7; Length 195;
Best Local Similarity 23.4%; Pred. No. 0.48;
Matches 29; Conservative 15; Mismatches 37; Indels 43; Gaps 5;

```

```

QY 3 IMEIFITGLLGASLLSIGPQNVLVV-----KQIKRE-----GLIIVLVCLISD 49
DB 5 LLSAFMTVYLLITR--MTGPNMIIILSSATSHGFRQSTRVLGMSLGLIIVLVCLISD 61
QY 50 VFLFAGTIGVLDLSNAPRIVDIMEWGIAVYLLMFVAVMAAKDAMTKVEAPQIIEETPT 109
DB 62 FSLAVIDPAVAVHLLS-----WAGAAVIVMIAWKIA-----TSP 94
QY 110 TVPD 113
DB 95 TKED 98

```

```

RESULT 8
US-10-449-902-53836
; Sequence 53836, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 53836
; LENGTH: 597
; TYPE: prt
; ORGANISM: Oryza sativa
US-10-449-902-53836

```

```

Query Match      12.2%; Score 75.5; DB 6; Length 597;
Best Local Similarity 20.8%; Pred. No. 3;
Matches 30; Conservative 22; Mismatches 53; Indels 39; Gaps 4;

```

```

QY 12 LIGASLLSTIGPQNVLVKQIKREGLIIVLVCLISDVFLFAGTIGVLDLSNAPRIVL 71
DB 197 VLGSAHLVSSAVLVGIVGVNLGARG--VAVRDVDFRDSFLAALAAVAVVLAAGEVIT 253
QY 72 DIMRWGIAVYLLMFVAVMAAKDAMTN-----KYAPQIIEETPT 108
DB 254 ----WGALAFSTLYVYVVAVAFTHGRAPRSKGGAGADHTADAFSELGVNAETKFFYGDDE 309
QY 109 PTVPDPPTLV-----GVFGGG 123
DB 310 PLLPDTAPLLSYYPGDDGDDGGGG 333

```

```

RESULT 9
US-10-449-902-33208
; Sequence 33208, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 33208
; LENGTH: 223
; TYPE: prt
; ORGANISM: Oryza sativa
US-10-449-902-33208

```

```

Query Match      11.8%; Score 73; DB 6; Length 223;
Best Local Similarity 23.5%; Pred. No. 1.7;
Matches 24; Conservative 24; Mismatches 40; Indels 14; Gaps 5;

```

```

QY 6 IFITGLLGASLLSIGPQNVLVKQIK--REGLIIVLVCLISDVFLFAGTIGVLDL 62

```

Db 105 IALGLLIMPELL-VATTNAVVSVMLSLAAGSFLMFACILVA-VYI---GVVSVAV 159  
 QY 63 LSNAPVLDIM-----RMGIAVLMFAVMAKADANTKV 98  
 Db 160 FVISAIVISAIVGMATGMLGFFFMIMFAARKSDLTKHSI 201

## RESULT 10

US-10-449-902-38726  
 ; Sequence 38726, Application US/10449902  
 ; Publication No. US20060123505A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: National Institute of Agrobiological Sciences.  
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
 ; APPLICANT: The Institute of Physical and Chemical Research.  
 ; APPLICANT: Foundation for Advancement of International Science.  
 ; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
 ; FILE REFERENCE: MOA-A0205Y1-US  
 ; CURRENT APPLICATION NUMBER: US/10/449,902  
 ; PRIOR FILING DATE: 2003-05-29  
 ; PRIOR APPLICATION NUMBER: JP 2002-203269  
 ; PRIOR FILING DATE: 2002-05-30  
 ; PRIOR APPLICATION NUMBER: JP 2002-383870  
 ; PRIOR FILING DATE: 2002-12-11  
 ; NUMBER OF SEQ ID NOS: 56791  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 38726  
 ; LENGTH: 594  
 ; TYPE: PRT  
 ; ORGANISM: Oryza sativa  
 ; US-10-449-902-38726

Query Match 11.8%; Score 73; DB 6; Length 594;  
 Best Local Similarity 29.6%; Pred. No. 5.5;  
 Matches 29; Conservative 14; Mismatches 29; Indels 26; Gaps 6;

QY 4 MEIFITGLLIGASLLSLISGPONVVIKQIKREGLIAVLV-----CLISD-----V 50  
 Db 192 LSLFVAGYGLGPIPLM---GP-----LSQYGRPRPFITGAMLVYCFNIGCALSKRTGSLIV 244  
 QY 51 FLFIAGTGLVDLSNAPVLDIMRWG---GIAYLIW 84  
 Db 245 FRLAGTFAPASPLTNSGVIAIDL--WDKTRGIALSLIF 280

## RESULT 11

US-10-471-571A-822  
 ; Sequence 822, Application US/10471571A  
 ; Publication No. US20060115490A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHIRON SPA  
 ; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS  
 ; FILE REFERENCE: P026927WO  
 ; CURRENT APPLICATION NUMBER: US/10/471,571A  
 ; CURRENT FILING DATE: 2003-09-12  
 ; PRIOR APPLICATION NUMBER: GB-0107661.1  
 ; PRIOR FILING DATE: 2001-03-27  
 ; NUMBER OF SEQ ID NOS: 5642  
 ; SOFTWARE: Seqwin99, version 1.03  
 ; SEQ ID NO 822  
 ; LENGTH: 432  
 ; TYPE: PRT  
 ; ORGANISM: Staphylococcus aureus  
 ; FEATURE:  
 ; NAME/KEY: MISC\_FEATURE  
 ; LOCATION: (1)..(432)  
 ; OTHER INFORMATION: aeenical pump membrane  
 ; US-10-471-571A-822

Query Match 11.7%; Score 72.5; DB 6; Length 432;  
 Best Local Similarity 31.1%; Pred. No. 4.3;  
 Matches 23; Conservative 7; Mismatches 19; Indels 25; Gaps 3;

QY 19 LSLGPNVVIKQIKREGLIAVLVCLISDVFLIAGTGLVDLSNAPVLDIMRWG 78  
 Db 350 IALGOSNV---HGMLEGLI-----YANVIGSDLGPKITPI-----GS 384  
 QY 79 IAYLMFAVMAKAD 92  
 Db 385 LATLMLHVLTKKD 398

## RESULT 12

US-11-056-355B-24250  
 ; Sequence 24250, Application US/11056355B  
 ; Publication No. US20060150283A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brover, Vyacheslav  
 ; APPLICANT: Alexandrov, Nikolai  
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
 ; FILE REFERENCE: 2750-1590PUS2  
 ; CURRENT APPLICATION NUMBER: US/11/056,355B  
 ; CURRENT FILING DATE: 2005-02-14  
 ; PRIOR APPLICATION NUMBER: 60/544,190  
 ; PRIOR FILING DATE: 2004-02-13  
 ; NUMBER OF SEQ ID NOS: 119966  
 ; SEQ ID NO 24250  
 ; LENGTH: 272  
 ; TYPE: PRT  
 ; ORGANISM: Arabidopsis thaliana  
 ; FEATURE:  
 ; NAME/KEY: peptide  
 ; LOCATION: (1)..(272)  
 ; OTHER INFORMATION: Ceres Seq. ID no. 12321538  
 ; US-11-056-355B-24250

Query Match 11.5%; Score 71; DB 7; Length 272;  
 Best Local Similarity 28.5%; Pred. No. 3.6;  
 Matches 37; Conservative 23; Mismatches 50; Indels 20; Gaps 7;

QY 7 FITGL-----LIGASLLSLISGPONVVIKQIKREGLIAVLVCLISDVFLIAGTGLV 60  
 Db 7 FVAGLNTLMVLVGS---AIGSIYMFVHQGV-IDCESAIRPLTLTGLIFLVSILGV 62  
 QY 61 ---DLSNAPVLDIMRWGIAVLMFAVMAKADMTKVEAPDIE---ETEPVVD 113  
 Db 63 ISGCFKENLAMSYYLILFGLVIALMTISIFL--FVTK-GAGRVSGRGKRYRTVD 119  
 QY 114 DTPLGVFGG 123  
 Db 120 STMWNGFVG 129

## RESULT 13

US-10-471-571A-4172  
 ; Sequence 4172, Application US/10471571A  
 ; Publication No. US20060115490A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHIRON SPA  
 ; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS  
 ; FILE REFERENCE: P026927WO  
 ; CURRENT APPLICATION NUMBER: US/10/471,571A  
 ; CURRENT FILING DATE: 2003-09-12  
 ; PRIOR APPLICATION NUMBER: GB-0107661.1  
 ; PRIOR FILING DATE: 2001-03-27  
 ; NUMBER OF SEQ ID NOS: 5642  
 ; SOFTWARE: Seqwin99, version 1.03  
 ; SEQ ID NO 4172  
 ; LENGTH: 338  
 ; TYPE: PRT  
 ; ORGANISM: Staphylococcus aureus  
 ; FEATURE:  
 ; NAME/KEY: MISC\_FEATURE  
 ; LOCATION: (1)..(338)

OTHER INFORMATION: ferrichrome transport  
US-10-471-571A-4172

US-10-471-571A-4172

Query Match	11.4%	Score	70.5	DB	6	Length	338
Best Local Similarity	24.5%	Pred	No. 5.3				
Matches	25	Conservative	22	Mismatches	40	Indels	15
						Gaps	3

Dy 1 MWMEFITGLLGASLLISGQNVL-----IKGIKREGIAY-----LVLCI 47  
:::|::|::|::|:  
Db 11 LIALAVFSILFLGCTWSITSGEYNIPIVERFFKTLIGGDAIDELILLDFRLPRMWTIL 700

QY 48 SDVLEFIAGTLGVDDLNS--AAPIVLDIRMGGIAIYLLMPAV 87  
 : | | : : | | | | : : :  
 Db 71 AGAALSISGAIVQSVTKNPFAEPGILGINAGGFAIALFLAI 112

RESULT 14  
US-11-174-307B-70  
Sequence 70. Application US/11174307B

Publication No. US20060143729A1  
GENERAL INFORMATION:  
APPLICANT: ALEXANDROV, Nikolai  
APPLICANT: BROVER, Vyacheslav

```

; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
;
; TITLE OF INVENTION: NUCLEOLIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
;
; TITLE OF INVENTION: NUCLEOLIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
;
; FILE REFERENCE: 2750-1601PUS2
;
CURRENT APPLICATION NUMBER: US/11/174.307B

```

```

LOCATION:
OTHER INFORMATION: GI Number: 61658325; NR Description: 'cation/H+ exchanger'
US-11-174-307B-70

```

QY 4 MEIFITGILLGASLLLSIGPQNVLVIKQGIKRREGIALLVLCISDFELFIAGTLGVDLL 63  
::: ||| :::: : | | : : : :  
Db 356 IEDLVMGILLPLYFVMS-GLKTIDITTIQGVKSMGRALAVI--TACFGKIIVGTVSALL 411

Db

Oy	64	SNA---APVLDI-MRWGAIYLL-----WAVMAADAMTNVEAEQIIIE	105
		:: :	
	412	CKVRLRESVVLGVLMNTKGLVELLIYNIGDKRKLVSDDQTAFIMVMMAIFTFITTPIVLA	471

```

qy      106 ETEPIVDDT 115
          :|:
Db      472 LYKPSSETQT 481

```

RESULT 15  
US-11-056-355B-100151  
: Sequence 100151, Application US/11056355B

1. PUBLICATION NO.: 0320050150253A1  
 2. GENERAL INFORMATION:  
 3. APPLICANT: Brover, Vyacheslav  
 4. APPLICANT: Alexandrov, Nickolai  
 5. TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
 6. TITLE OF INVENTION: Polypeptides Encoded Thereby  
 7. FILE REFERENCE: 2750-1580PUS2  
 8. CURRENT APPLICATION NUMBER: US/11/056,355B  
 9. CURRENT FILING DATE: 2005-02-14  
 10. PRIOR APPLICATION NUMBER: 60/544,190  
 11. PRIOR FILING DATE: 2004-02-13  
 12. NUMBER OF SEQ. ID NOS: 119966  
 13. SEQ. ID NO 100151  
 14. LENGTH: 271  
 15. TYPE: DYE  
 16. ORGANISM: Arabidopsis thaliana  
 17. FEATURE:  
 18. NAME/KEY: peptide  
 19. LOCATION: (1)-(271)  
 20. OTHER INFORMATION: Ceres Seq. ID no. 13604468  
 21. US-11-056-355B-100151

Query Match	11.1%	Score 69	DB 7	Length 271
Best Local Similarity	28.5%	Pred. No. 5.9		
Matches 37	Conservative 23	Mismatches 50	Gaps 20	Gaps 7

[illegible]

```
Search completed: July 19, 2006, 00:46:52
Job time : 29 secs
```